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July 25, 2004, 09:54:25; Search time 987 Seconds (without alignments) 7503.317 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                          3216467 seqs, 2444149694 residues
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                                                                                          OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                         Sequence:
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Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl	Sequence 433, App	Sequence 55, Appl	Sequence 9, Appli	Sequence 43, Appl	Sequence 7, Appli	Sequence 41, Appl	Sequence 14, Appl	Sequence 53, Appl	Sequence 57, Appl	Sequence 7, Appli	Sequence 8, Appli
ΩΙ	US-10-135-689-1	US-10-690-617-1	US-10-333-314-39	US-10-302-172-433	US-10-092-900A-55	US-09-922-138-9	US-10-391-364-43	US-09-922-138-7	US-10-391-364-41	US-10-168-582-14	US-10-092-900A-53	US-10-092-900A-57	US-10-316-124-7	US-10-316-124-8
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% Query Match Length DB	2190	2190	1937	2018	1611	1683	1686	2711	2711	3501	1547	1725	4427	4427
% Query Match	100.0	100.0	7.66		99.4									
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Gaps

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Indels

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Best Local Similarity 100. Matches 1515; Conservative 232

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61 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 120

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92 Pp

1 ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGGGTAGAACGGGTG

100.0%; Score 1515; DB 14; Length 2190; 100.0%; Pred. No. 0;

121 GGTGTGGACCCCCCACCACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA 180

Sequence 51, Appl	53	113	22,		e 18;	20	23	'n		84	24.	16.	Sequence 1271, Ap	56	2780		22375		603,	1603	8	92,	Λì	192,	Sequence 1333, Ap	ò	15808,	m	59939,	m
US-10-205-823-51	-205-823-5	-10-295-0	41-2	-764-868-2	-09-764-875-1	US-10-296-115-20	841-	689	US-10-690-617-3	97	Π	245	US-09-918-995-1271	7#	US-09-918-995-2780	US-09-864-761-5606	64-761-2237	5-720	US-09-764-869-1603	US-10-091-504-1603	17		US-10-091-504-192	577-19	-09-954-456-133	9-880-107-	US-10-425-114-15808	US-10-425-114-33104	US-10-437-963-59939	US-10-425-114-3580
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43.0	43.0	43.0	42.4	35.0	35.0	34.9	34.2	23.8	23.8	23.4	23.0	18.0	17.3	16.3	16.1	13.3	13.3	9.4	9.2	9.5	9.2	0.6	9.0	9.0	7.5	7.5	7.5	7.3	7.0	7.0
651.2	651	651	643	529.6	529.6	529	518	361	361	354.4	348.8	272	262.6	246.8	244.6	201.2	201	142.8	139	139	139	136.8	136.8	136.8	113.8	113.8	113.8	110.8	106	106
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WESULA Sequence 1, Application US/10135689 Sequence 1, Application US/10135689 Publication No. US20020123121A1 GENERAL INFORMATION: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES; CURRENT FILING DATE: 2000-05-01 PRIOR PILING DATE: 2000-11-13 PRIOR FILING DATE: 2000-11-13 PRIOR FILING DATE: 2000-12-06 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 2190 TAPNISM: Home sapiens US-10-135-689-1

ALIGNMENTS

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CTGGTGAAAGAAGGGTTTTGGTGAAGGGGGCAAGAGCCCCAGGAGCTCCCCGGCGTCCAGGAA 1500
                              1613 CTGGTGAAAGAAGGTTTGGTGAAGGGGGCAAGAGCCCAGAGGTCCCCGGCGTCCAGGA 1672
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GRENERAL INFORMATION:
APPLICANT: RAIN, FAITAN A.; GURURAJAN, Rajagopal
APPLICANT: HARALIA, April J.A.; CHAMLA, Narinder K.
APPLICANT: ARVIZU, Chandra S.; CHAMLA, Narinder K.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: BAUGHN, Mariah R.; POLICKX, Jennifer L.
APPLICANT: HANDY, Mariah R.; POLICKX, Jennifer L.
APPLICANT: HANDY, Mariah R.; POLICKX, Jennifer L.
APPLICANT: HOUVEN, Danniel B.; LU, Yan
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
APPLICANT: KERNWALD, SATA R.; TANG, Y. Tom
APPLICANT: KERNWALD, SATA R.; TANG, Junming
APPLICANT: GREENWALD, SALR, ROGERICY T.
APPLICANT: MANGER: US 60/220,038
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL PROGRAM
TENNYTH. 1037
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Pred. No. 0;
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b; OTHER INFORMATION: Incyte ID No: 2190612CB1
US-10-333-314-39
                                                                                                                                                                                                  US-10-333-314-39
; Sequence 39, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
                                                                                                         1673 GACGAGGCTGCATCC 1687
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Best Local Similarity 99.8
Matches 1512; Conservative
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ORGANISM: Homo sapiens
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CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG
                                                         GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC
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Db 1325 GAGGAGCACTGCAGGTGACGAGGAGGAGGTAAGAACTCAGTCAG	March 19712-133 March 197120172
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Encoding Same

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1192 GAĞCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG 1251
                     GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGAACCCCCAGCATTCATGGCCCCCGAG
                                        GAGGGAACGACGCTCAGCTGTCCAGCACGGGGGAACCCCAGCATCATGGCCCCCGAG
                                                                                                         GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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US-09-202-138-9
| Sequence 9, Application US/09922138
| Sequence 9, Application US/09922138
| Patent No. US20020061574A1
| GENERAL INFORMATION:
| APPLICANT: Melvers, Rachel APPLICANT: Millonnium Pharmaceuticals, Inc. APPLICANT: Silos-Santiago, Irmaculada ITILE OF INVENTION: 16558, 14223, AND 16002, NOVEL HUMAN ITILE OF INVENTION: RINAGES AND USES THEREFOR FILE REFERENCE: 38155-20030.00
| CURRENT APPLICATION NUMBER: US/09/922,138 |
| CURRENT APPLICATION NUMBER: US/09/922,138 |
| PRIOR APPLICATION NUMBER: US/09/922,138 |
| PRIOR APPLICATION NUMBER: US/09/922,138 |
| NUMBER OF SEQ ID NOS: 38 |
| SOFTWARE: FASTSEQ FOR Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                    Score 1505.4;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                      99.4%;
99.6%;
                                                                                                                                                                    Query Match
Best Local Similarity 99.6
Matches 1509; Conservative
                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                  ; NAME/KEY: CDS
; LOCATION: (52)..(1567)
US-10-092-900A-55
NUMBER OF SEQ ID
                 SEQ ID NO 55
LENGTH: 1611
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	WESULT 7 US-10-391-364-43 US-10-391-391-391-391-391-391-391-391-391-391
ATGGAGGGGGTCCAGCTGTCTGCTGCCAGATCCTCGGGCAGACTGGTAGAACGGGTG 60 ATGGAGGGGGTCCAGCTGTCTGCTGCCAGATCCTCGGGCAGACTGGTAGAACGGGTG 60 ATGGAGGGGGTCCAGCTGTCTGTGTCTGCCCAGAGCCTGTAGAACGGTG 60 GCAGCCATCGATGTGACTCACTTGGAGGACCAGAGCCTACTAGAAAC 120 H	481 ANAMGANGTTACTGAAGCAGTATCCAGGGGGCCCCCCCGAAGAGGGTCCCAG

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1381 AACCCGTTTGAGCCCCCAAGCACGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTA 1440
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      GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGAACCCCAGCATTCATGGCCCCCGAG
                        GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGGAACCCCCAGCATTCATGGCCCCCCGAG
                                                                     GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCCACTGGC
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Patent No. US20020061574A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 16568, 14223, AND 16002, NOVEL HUMAN
TITLE OF INVENTION: KINASES AND USES THEREFOR
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CURRENT PELING DATE: 2001-1.28
PRIOR APPLICATION NUMBER: US/09/922,138
PRIOR PLING DATE: 2001-1.28
PRIOR PLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
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; NAME/KBY: misc feature
; LOCATION: (1)...(2711)
; OTHER INFORMATION: n = A,T,C o
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ORGANISM: Homo sapiens
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.larity 99.4%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Similarity
Matches 1496; Conserv
LENGTH: 1686
TYPE: DNA
ORGANISM: Homo s:
FEATURE:
                                                                                NAME/KEY: CDS
LOCATION: (1)
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QY 1021 GTCACGTTGTACTGGGAAGTGCCCATTCATCGACGATTCATCCTGGCC 1080 Db 1218 GTCACGTTGTACTTGTCTATGGGAAGTGCCCGTTCATCGACGATTTCATCCTGGCC 1277 QY 1081 CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCCAGAAATCAGCGAG 1140	1278 CTCCACAGGAAGATCAGAATGAGCCGTGGTTTTCCTGAGGGGCCAGAAATCAGCGAGGGCGAGGGGCCAGAAATCAGCGAGGGCGAGGGCGAGGGCGAGGAGGGGGGGG	1338 GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGGGAGACGAGAATTGGGGTG 1201 CCAGACATCAAGTTGCACCCTTGGGTGACCAAGAACGGGGAGGAGCCCCTTCCTT	1261		1578 AACCGTITGAGCCCCAAGCAGGGAAGAGCGATCCATGTCTGCTCCAGGAACCTA	141 CIGGIGAAAGAAGGGITIGGIGAAGGGGGAAGAGCCCAGAGCICCCCGGCGICCAGGACICAGACICCAGGACICAGACACACAC	TACCA 170	RESULT 9 US-10-391-364-41 ; Sequence 41, Application US/10391364 ; bulliantion NS TROSOMAN 1313034	; GENERAL INFORMATION: ; APPLICANT: Millennium Pharmaceuticals, Inc. ; APPLICANT: Meyers, Rachel E.	; APPLICANT: COLK, William James ; APPLICANT: Kapeller-Libermann, Rosana ; APPLICANT: Weich, Nadine S.	; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352, 1TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND 1TITLE OF INVENTION: USES THEREFOR 11111 DEPROPERMENT OF THE OF	; FILE REFERENCE: PRIOS-OLD-OMAIN; CURRENT APPLICATION NUMBER: US/10/391,364; CURRENT FILING DATE: 2003-03-18; PRIOR APPLICATION NUMBER: US 09/950,370	; PRIOR FILING DATE: 2001-09-10; PRIOR PAPLICATION NUMBER: US 60/231,084; PRIOR FILING DATE: 2000-09-08; PRIOR APPLICATION NUMBER: US 10/294,039	; PRIOR FILING DATE: 2002-11-13; PRIOR FILING DATE: 2001-11-13; PRIOR APPLICATION NUMBER: US 10/266,035	; FRIOR FILING DATE: 2002-10-0/; PRIOR PAPLICATION NUMBER: US 60/328,198 ; PRIOR FILING DATE: 2001-10-09 ; PRIOR APPLICATION NUMBER: US 09/717,926	
 s; Score 1490.6; DB 9; Length 2711; b; Pred. No. 0; 0; Mismatches 9; Indels 0; Galmarrangeraggest and consequences 	198 AIGGAGGGGTCCAGCTGTCTGCCCCAGGATCCTCGGGCAGAGCTGGTGGAGGGGGGGG	Db 258 GLAGCCATCGATGATGATGATGATGATGATGATGATGATGATGATGATG	OY 181 CTGCTCCAGCCCGGCCTAGCCTCTCAGCAGGAAGCTTTCCCTACAGGAGGGCCAGCA 240	OY 241 GGAAGCTATCTGGAGGCGCAGGCCTTATGCCACGGGGCCTGCCAGCCA	Qy 301 CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG 3.60 Db 4.98 CCCCGGGCCTGGCGAGGCCCACCATCGAGTCCCACCACCACCACCACCATCTCAGATGCAGAG 5.57	OY 361 GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 420 	QY 421 GTGGTGAGGCTGCCTACAAAGTGAAGGACACACATATGCAATGAAAGTCCTTTCC 480	QY 481 AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGAGAGGGTCCCAG 540	Qy 541 GCTGCCCAGGGAGGACCAGCCAGCAGCTGCCCCTGGAGCGGGTGTACCAGGAGATT 600 Db 738 GCTGCCCAGGGAGCACCAGCCAGCTGCCCCTGGAGCGGGTGTACCAGGAGTT 797	OY 601 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 660	Qy 661 CCAGCTGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA 720 	OY 721 GIGCCCIGIGACAAGCCCITCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCAIC 780	Oy 781 CIGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC 840	QY 841 CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT 900 DD 1038 CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT 1097	QY 901 GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGGAACCCCAGCATTCATGGCCCCCGAG 960	OY 961 GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC 1020

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APPLICANT: LAL, Preeti
APPLICANT: KAHN, FAZTAN A.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0002 PCT
CURRENT APPLICATION NUMBER: US/10/168,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/10168582; Publication No. US20040058426A1 GENERAL INFORMATION:
APPLICANT: YANG, Junming APPLICANT: BAUGHN, Mariah R. APPLICANT: BURRORD, Neil APPLICANT: BURRORD, Neil APPLICANT: RUBDY, Roopa APPLICANT: RUBDY, Roopa APPLICANT: RUBL Henry
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PRIOR FILING DATE: 2001-10-09
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SCFUMARE: Factor of Windows Version 4.0
SEQ ID NO 41
LENGTH: 2711
TYPE: DNA
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FEATURE:
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FEATURE:
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; Sequence 53, Application US/10092900A
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; GENERAL INFORMATION:
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Li, Li, Li, Li, Branch.
APPLICANT: Li, Li, Li, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gran, Eryan D.
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APPLICANT: Gangolli, Esha A.
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APPLICANT: Geo, Xiaojia Sasha
APPLICANT: Tchernev, Velizar T.
APPLICANT: Fernandes, Elma R.
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CURRENT FILING DATE: 2002-06-20
PRIOR PAPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
NUMBER OF SEQ ID NOS: 24
SCFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 3501
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; OTHER INFORMATION: Incyte ID No. US20040058426A1 2041716CB1
US-10-168-582-14
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                                                                              APPLICANT: Liu, XI David W. APPLICANT: Liu, XI David W. APPLICANT: Spaderna, Steven K. APPLICANT: Spaderna, Steven K. APPLICANT: Catterno, Elina APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Lepley, Denise W. APPLICANT: No. U020040043382Alel Proteins and Nucleic Acids Encoding Same APPLICANT: Blager, Daniel W. U020040043382Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21012-236C CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: USSN 60/274,281

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR PRILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-18

PRIOR APPLICATION NUMBER: USSN 60/294,899

PRIOR APPLICATION NUMBER: USSN 60/294,899
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PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
SEQ ID NO 53
LENGTH: 1547
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Pred. No. 0;
0; Mismatches
                           Malyankar, Uriel M.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.5%;
Matches 1492; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-10-092-900A-53
                                                                            Liu, Yi
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                                                                                                                                                                                                                    DB 13; Length 1725;
                                                                                                                                                                                                                                                                6; Indels 114;
                                                                                                                                                                                                               Score 1381.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                0; Mismatches
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92.6%;
                                                                                                                                                                                                                                                                Matches 1509; Conservative
                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                           ; LOCATION: (52) ... (1681) US-10-092-900A-57
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                  NAME/KEY: CDS
SEQ ID NO 57
LENGTH: 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, David W. APPLICANT: Spaderra, Steven K. APPLICANT: Spaderra, Steven K. APPLICANT: Spaderra, Steven K. APPLICANT: Catterton, Elina APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Leite, Mario W. APPLICANT: Alsobrook, John P. APPLICANT: Lepley, Denise M. APPLICANT: Lepley, Denise M. APPLICANT: Rieger, Daniel K. APPLICANT: Rieger, Daniel K. APPLICANT: Rieger, Daniel K. APPLICANT: Rieger, Daniel K. APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: NO. US20040043382Alel Proteins and Nucleic Acids Encoding Same TITLE OF INVENTION: NO. US20040043382Alel Proteins and Nucleic Acids Encoding CURRENT FILING DATE: 2002-03-07
CURRENT FILING DATE: 2001-03-08
FRIOR PLILING DATE: 2001-04-13
FRIOR APPLICATION NUMBER: USSN 60/238,092
FRIOR FILING DATE: 2001-03-08
FRIOR PARTOR PAR
                                                                                  CIGGIGAAAGAAGGGITIGGIGAAGGGGCAAGAGCCCAGAAGTCCCCGGCGICCAGGAA 1513
  AACCCGITTGAGCCCCAAGCACGGAGGAAGAGCGAICCAIGTCIGCICCAGGAAACCIA 1453
                                               CTGGTGAAAGAAGGGTTTTGGTGAAGGGGGCAAGAGCCCCAGAGCTCCCCGGCGTCCAGGAA
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PRIOR APPLICATION NUMBER: USSN 60/287,424
PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/10092900A Publication No. US20040043382A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Spytek, Kimberly A.
Shenoy, Suresh G.
Taupier Jr., Raymond J.
Pena, Carol E.A.
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Tchernev,, Velizar T.
Fernandes, Elma R.
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
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Zerhusen, Bryan D.
Gusev, Vladimir Y.
Ji, Weizhen
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Gangolli, Esha A.
Vernet, Corine A.M.
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Malyankar, Uriel M.
Gerlach, Valerie
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Miller, Charles E.
Kekuda, Ramesh
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Pena, c.
Li
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                                 DB 15;
                               Score 651.2; DB 15.
Pred. No. 4.3e-181;
0; Mismatches 348;
                               43.0%;
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Conservative
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Matches 873; Conser
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1 Sequence 7, Application US/10316124

2 Sequence 7, Application US/10316124

3 Sequence 7, Application US/20030152574A1

4 GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph

APPLICANT: Chun, Miyoung

7 TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210

8 FILE REFERENCE: MP101-29.PIRM

9 CURRENT APPLICATION NUMBER: US/10/316,124

9 CURRENT FILING DATE: 2002-12-10

9 PRIOR FILING DATE: 2001-12-10

9 NUMBER OF SEQ ID NOS: 9

10 SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                            CTGGGGGATGATGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTTGAGGGG
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ORGANISM: Homo sapiens
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Sequence 51, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Galat, Karen
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                                                     GGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCCAGGCACGGAG 1406
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APPLICANT: Chun, Miyoung
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
FILE REFERENCE: MPIO1-291P1RM
CURRENT APPLICATION NUMBER: US/10/316,124
CURRENT PILLIG DATE: 2002-12-10
PRIOR FILLIG DATE: 2001-12-10
PRIOR FILLIG DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                       GACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCCAGCTGGACCACGGTGATCCT
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                                                                                                                                                                                                                                                                                                                                                                   GGGCAAGAGCCCAGAGCTCCCCGG 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10316124 Publication No. US20030152574A1 GENERAL INFORMATION:
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APPLICANT: Znao, Aumen
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: MOYEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AUTILE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TILLE OF INVENTION: MAN BER: US,10/205,823
CURRENT PILING DATE: 2002-07-25
PRIOR PELLOATION NUMBER: 60/307,982
PRIOR PELLOATION NUMBER: 60/307,982
PRIOR PELLOATION NUMBER: 60/307,925
PRIOR PELLOATION NUMBER: 60/325,020
PRIOR PELLOATION NUMBER: 60/341,746
PRIOR PELLING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-13
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 455
SEQ ID NO 51
FENALTH 4442
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Pred. No. 4.5e-181;
0; Mismatches 348;
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Best Local Similarity 71.35
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Zhao, Xumei
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time : Search

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                                                                                                                                                                                                             CCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGTAAGATCAAGAGTCAGGC
                                        caccaradacaccacacaratada da cacacacacacacacaca da da cacacada da cara
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  CACGGCGGGAACCCCCAGCATTCATGGCCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTT
                                                                                          CAGTGGGAAGGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTTGTCTATGG
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein July 12, 2004, 04:23:48; Search time 57 Seconds Run on:

(without alignments)
852.223 Million cell updates/sec

US-10-690-617-2

2634

1 MEGGPAVCCQDPRAELVERV......FGEGGKSPELPGVQEDEAAS **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

505

283366 segs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched: hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1 2 6 4 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ca2+/calmodulin-de	Ca2+/calmodulin-de	calcium/calmodulin	probable Ca2+/calm	serine/threonine-p	protein kinase PAK	serine/threonine-p	probable serine/th	related to protein	probable serine/th	probable serine/th	serine/threonine-s	probable serine/th	probable serine/th	serine/threonine-s	probable serine/th	SNF-related kinase	hypothetical prote	probable protein k	probable protein k	serine/threonine-s	protein kinase (EC	probable serine/th	serine/threonine p	probable protein k	probable serine/th	probable serine/th	serine/threonine-s	probable carbon ca
SUMMARIES	ID	A57156	JC5669	JE0191	T37317	S58666	850632	T47464	S57252	T51085	T14736	T14735	A56009	T14822	T07788	JC1446	T10449	B90100	E85362	C84667	E84707	T52633	S52242	T18611	T50802	B84644	A86427	T07415	A26030	T41587
	DB	7	7	7	~	7	~	~	7	7	~	7	Н	7	7	Н	7	~	N	7	~	N	7	7	~	7	7	7	7	7
	Length	505	587	417	357	652	1142	382	260	1246	440	440	511	461	512	512	504	472	441	441	435	512	389	1192	445	469	480	504	633	576
d	Query Match	93.1	56.7	55.9	39.6	23.5	21.5	19.4	19.3	17.8	17.0	16.6	16.6	16.5	16.3	16.2	16.1	15.9	15.8	15.8	15.7	15.7	15.6	15.5	15.5	15.4	15.4	15.4	15.3	15.3
	Score	2452	1494	1472.5	1043	620	266	512	507.5	468	448	437	436.5	434			423.5	418.5	416.5	415.5	413.5	412.5	410	409.5	409	406.5	406	405.5	403.5	403
	Result No.	1	7	e	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps ..

Length 505;

Query Match 93.1%; Score 2452; DB 2; Length 5 Best Local Similarity 93.1%; Pred. No. 3.3e-101; Matches 470; Conservative 11; Mismatches 24; Indels

9 9 241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300

61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120

61 PTPVRPSLSARKFSLQERPAESCLEAQVGPYSTGPASHMSPRAWRRPTIESHHVALSDTE

g

1 MERSPAVCCODPRAELVERVAAISVAHLEEAEEGPEPASNGVDPSPRARAASVIPGSASR

1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR

δ g ò 121 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180

121

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31 401 15.2 473 1 \$59941 32 399.5 15.2 1246 2 \$699287 33 399.5 15.1 350 2 T06107 34 398.5 15.1 489 2 T04862 35 397.5 15.1 602 527513	serine/threonine-s protein H39E23.1 [
399.5 15.2 1246 2 399 15.1 350 2 398 15.1 489 2 397 5 15.1 489 2 397 5 15.1 600 2 399 6 39	protein H39E23.1 [
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398.5 15.1 489 2	bropante serme/ cu
	probable serine/th
1	FOG2 protein - yea
397 15.1	protein T25K16.13
	myosin-light-chain
394.5 15.0	probable protein k
394.5 15.0	Ca2+/calmodulin-de
	hypothetical prote
648 1	protein kinase (EC
42 393.5 14.9 887 2 T20941	hypothetical prote
	p69Eg3 protein - A
14.9	SNF1-related prote
45 391 14.8 445 2 TO9903	serine/threonine-s

KESUDI. I
A57156
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat
N/Alternate names: CaM-kinase kinase; microtubule-associated protein 2 kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: A57156; JC4789
R; Tokumitsu, H.; Enslen, H.; Soderling, T.R.
J. Biol. Chem. 270, 19320-19324, 1995
A; Title: Characterization of a Ca(2+)/calmodulin-dependent protein kinase cascade. Molec
A; Reference number: A57156; MUID: 95370263; PMID: 7642608
A;Accession: A57156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <tok></tok>
A; Cross-references: GB:L42810; NID: 9986940; PIDN: AAC42070.1; PID: 9986941
R;Okuno, S.; Kitani, T.; Fujisawa, H.
J. Biochem. 119, 1176-1181, 1996
4/Title: Evidence for the existence of Ca2+/calmodulin-dependent protein kinase IV kinase
A; Reference number: JC4789; MUID:96425004; PMID:8827455
A;Accession: JC4789
A;Molecule type: mRNA
A:Residues: 1-44,'P',46-80,'G',82-505 <oku></oku>
A;Cross-references: GB:AB023658; NID:g4512333; PIDN:BAA75246.1; PID:g4512334
A; Experimental source: brain
C; Comment: This enzyme is a Ca2+-responsive multifunctional protein kinase. It plays role
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C: Keywords: ATP; brain; calmodulin binding; phosphotransferase; protein Kinase
F:126-140/Domain: procent Kinase Nombology KALN> F:134-140/Benion: profesin kinase MTD-hinding motif
TOTAL TARE MORNING THE PRINCIPLE WILLIAM WOLFE

Db 241 VPCDKPPEEGARLYLRDIILGIEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQP 300 301 EGNDAQLSSTAGTPAFNAPEAISDSGOSFSGKALDVNATGVTLYCFVYGKCPFIDDFILA 360 301 EGNDAQLSSTAGTPAFNAPEAISDSGOSFSGKALDVNATGVTLYCFVYGKCPFIDDFILA 360 301 EGNDAQLSSTAGTPAFNAPEAISDTGGSFSGKALDVNATGVTLYCFVYGKCPFIDDFILA 360 301 EGNDAQLSSTAGTPAFNAPEAISDTGGSFSGKALDVNATGVTLYCFVYGKCPFIDBFILA 360 301 LHRKIKNSPVYPPEEPEISEELKDLIILKMLDKNPFTRIGVPDIKLHPWYTKNGEEPLPSE 420 361 LHRKIKNSPVYPPEEPEISEELKDLIILKMLDKNPFTRIGVPDIKLHPWYTKNGEEPLPSE 420 421 EEHCSVVBYTEGEVKNSVKLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL 480 421 EEHCSVVBVTEGEVKNSVKLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL 480 421 LVKEGCGGGGGKSPELFGVQEDBAAS 505 481 LVKEGCGGGGGKSPELFGVQEDBAAS 505	Oy 406 HPWVTKNGEEPLPSEEBHCSVVEVTEGEVKNSVELIPSWTTVILVKSMLRKRSFGNPFEP 465
RESULT 2 JCS669 Ca2+/calmodulin-dependent protein kinase kinase (EC 2.7.1) beta chain - rat C;Species: Rattus norvegiums (Norway rat) C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999 C;Accession: JCS669; PC4493 R;Kitani, T.; Okuno, S.; Fujisawa, H. A;Kitani, T.; Okuno, S.; Fujisawa, H. A;Tile: Molecular cloning of Ca2+/calmodulin-dependent protein kinase kinase beta. A;Reference number: JC5669; MUID:97420710; PMID:9276695	A;Reference number: JE0191 A;Accession: UE0191 A;Accession: UE0191 A;Accession: UE0191 A;Accession: UE0191 A;Accession: UE0191 A;Residues: 1-417 < HSU> C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme functions as a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/calmodulin-driven sign C;Comment: This enzyme function is a key intermediaries in Ca2+/ca1-(ca2+/ca2+/ca2+/ca2+/ca2+/ca2+/ca2+/ca2+/
A; Accession: JC5669 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Accession: PC4493 A; Accession: PC4493 A; Accession: PC4493 A; Accession: PC4493 A; Accession: PC493 A; Molecule type: protein A; Residues: 425-501 <ki2> A; Residues: 425-501 <ki2> C; Superimental source: cerebellar C; Superimental source: cerebellar C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C; Keywords: ATP; phosphotransferase C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homolog C; Keywords: ATP; phosphotransferase B; 162-445/Domain: protein kinase homology <kin> A; 70-104/Nomain: protein kinase homology <kin-< td=""><td>Query Match 55.9%; Score 1472.5; DB 2; Length 417; Best Local Similarity 68.9%; Pred. No. 3e-58; Indels 1; Gaps 1; Matches 272; Conservative 72; Mismatches 50; Indels 1; Gaps 1; Qy 90 PYATGPASHISPRAMRRPITESHHVAISDACUQLNQYKLQSEIGKGAYGVVRLAYNES 149 Db 11 PYSPVSSPQSSPRLPRRPTVSSHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLAYNEN 70 Qy 150 EDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQBIAILKKLDHV 209 ::: 209 71 DNTYYAMKVLSKKKLIRQAGFPRRPPRGTRPAPGGCIQPRGFIEQVYQBIAILKKLDHP 130 Db 71 DNTYYAMKVLSKKKLIRQAGFPRRPPRGTRPAPGGCIQPRGFIEQVYQBIAILKKLDHP 130</td></kin-<></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></kin></ki2></ki2>	Query Match 55.9%; Score 1472.5; DB 2; Length 417; Best Local Similarity 68.9%; Pred. No. 3e-58; Indels 1; Gaps 1; Matches 272; Conservative 72; Mismatches 50; Indels 1; Gaps 1; Qy 90 PYATGPASHISPRAMRRPITESHHVAISDACUQLNQYKLQSEIGKGAYGVVRLAYNES 149 Db 11 PYSPVSSPQSSPRLPRRPTVSSHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLAYNEN 70 Qy 150 EDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQBIAILKKLDHV 209 ::: 209 71 DNTYYAMKVLSKKKLIRQAGFPRRPPRGTRPAPGGCIQPRGFIEQVYQBIAILKKLDHP 130 Db 71 DNTYYAMKVLSKKKLIRQAGFPRRPPRGTRPAPGGCIQPRGFIEQVYQBIAILKKLDHP 130
Fig. 137, Domain: Alf Dinding #Status predicted <cab> Fig. 137, Domain: Calmodilin-binding #Status predicted <cab> Query Match Watches 283; Conservative 75; Pred. No. 4.7-6-59; Indels 26; Gaps 3; Matches 283; Conservative 75; Mismatches 55; Indels 26; Gaps 3; Qy 64 ARPSLSARKLSLOERPAGSYLEAQAGPYATGPASHISPRAWR 105</cab></cab>	210 NVVKLIEVLDDPAEDNLYLVFDLLEKGPVMEVPCDKPFSEEGARLYLRDVILGIEYLHCO [
Db 89 SRSLLSGGKWSLQERSQGGPASSSSLDMNGRCICPSLSYSPASSPQSSPRWFR 141 Qy 106 RPTIESHHVAISDAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLL 165 : :	Oy 330 SGKALDWWATGYTLYCEVYGKOPFIDDFILALHRKIKNEPVVPEEPHISEELKDLILKM 389
226 LYLVFDLLRKGPVMEVPCDRPFSBEQARLYLRDVLGLBYLHOCKIVHRDIKPSNLLLGD	SULT 4 SULT 4 Substitute Supstitute Supstitute

Tue Jul

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A,Accession: S2632
A,Molecule type: DNA
A,Rocession: S2632
A,Molecule type: DNA
A,Cossidus: 1-1142
B,Hovland, P.G.; Sclafani, R.A.
Submitted to the EMBL Data Library, August 1994
A,Description: PAKI: DNA Polymerase Alpha Suppressing Protein Kinase.
A,Accession: S47952
A,Accession: S47952
A,Rollcule type: DNA
A,Residues: 1-170, 'H', 172-265, 'DS', 269-657, 'LD' <HOV>
A,Residues: 1-170, 'H', 172-265, 'DS', 269-657, 'LD' <HOV>
A,Coss-references: EMBL:U13398; NID:g53279; PIDN:AAC49840.1; PID:g532798
B,Mulligan, U.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, ENDMINGER: BMBL Data Library, February 1993
A,Accession: S43223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PTIESHHVAISDAEDCVQLNQYKLQSEIGKGAY 139
                                                                                                                                                                                                     ORLYSDNFQEAQROWKRLQEWGEVKETKKIRKRFDRFSGRK---YINHYEIIKELGRGMH 146
                                                                                                                                                                                                                                               GVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQE 199
                                                                                                                                                                                                                                                                                           147 GKVKLGRDTVTRELLAIKIIPKTE------RRP-----KLGRANASSQKEKVRRE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAFMAPEAI --- SDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHRKIKNEPV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPF---EPQARREERSMSAPGNLLVK 483
                                                                                                               89
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C;Species: Saccharomyces cerevisiae
C;Decies: Saccharomyce cerevisiae
C;Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S50632; S47952; S43223
R;Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981,
A;Reference number: S50437
                                                                                               IAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCDKP-FSEEQARLYLRD
                                                                                                                                                                                                                                                                                                                                                                                                                               VILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGNDAQLSSTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 VFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEP----LPSEEEHCSV
                           Gaps
                           78;
                           Indels
                                                                     SVIPGSTSRLLPARPSLSARKLSLQER--PAGSYLEAQAGPYATG-
  Pred. No. 1.3e-20;
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                           67;
    34.48;
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A; Residues: 1-176,'VYQIK'
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    Similarity
                           168;
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A;Experimental source: strain Bristol N2
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C;Keywords: ATP; brain; calmodulin binding; phosphotransferase; protein kinase
F;19-302/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: A novel protein Kinase gene ssp1(+) is required for alteration of growth polari A; Reference number: $5866; MUID:95354651; PMID:7628434
A; Accession: $58666
A; A; Accession: $58666
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-652 < MATP.
A; Cross-references: GB:D45882; NID:g1041184; PIDN:BAA08301.1; PID:d1008896; PID:g1041185
B; Purnelle, B.; Goffeau, A.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL049609; PIDN:CAB40783.1; GSPDB:GN00068; SPDB:SPCC297.03
A;Experimental source: strain 972h-; cosmid c297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFEGNDAQLSSTAGTPAFMAPEAISDSGQSF-SGKALDVWATGVTLYCFVYGKCPFIDDF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 IIALHKKIKNDPIVFPEAPILSEALQDIILGMLKKDPGHRLMLHEVKVHTWVTRDGTVPM 310
                                                                                                                                                                                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                                                                                                SESYIQINQYRLMEEIGGGSYGIVKLAYNEEDKNLYALKVLDKWKLLKNFACFRQPPFRR
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A;Reference number: Z21682; MUID:96210015; PMID:8631893
A;Accession: T37317
                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                 39.6%; Score 1043; DB 2; 57.2%; Pred. No. 1.9e-39;
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A;Accession: T41270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                       A;Accession: T37317
A;Kstuus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-357 <EDE>
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ATP-binding motif
                                                                                                                                                                                                                                                                                             64; Mismatches
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C;Keywords: ATP
F;133-409/Domain:
F;141-149/Region:
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A; Experimental source: strain S288C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Note: YGL179c
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; transmemb
F;48-344/Domain: protein kinase homology «KIN»
F;56-64/Region: protein kinase ATP-binding motif
F;256-272/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable serine/threonine-specific protein kinase (BC 2.7.1.-) YGL179c - yeast (Sacc Probable serine/threonine-specific protein G1618
C;Species: Saccharomyces cerevisiae
C;Date: 28-0ct-1995 #sequence revision 03-Nov-1995 #text_change 19-Apr-2002
C;Accession: S57252; S64196; S56168
R;Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Bruschi, C.V.
Yeast 11, 76-774, 1995
A;Itle: The DNA sequence of a 7941 bp fragment of the left arm of chromosome VII of ation and a putative serine/threonine protein kinase gene.
A;Reference number: S57252; MUID:95397594; PMID:7668046
A;Accession: S57252
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-560 <CCGA
A;Cross-references: EMBL:X83690; NID:9794143; PIDN:CAA58659.1; PID:9794144
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D. submitted to the Protein Sequence Database, May 1996
A;Accession: S64183
A;Accession: S64184
A;Accession: S64187
A;Cross-references: EMBL:Z77701; NID:91322788; PIDN:CAA96891.1; PID:e243787; PID:9133
                                                                                                                                                        338
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--VLREVMIMKTLEHPNIVNLIEVIDDPEFDD 177
                                                                                                                                                                                                                                         TGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRI 398
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                                                                                          287 VGVTLYCMILGQYPFLGDTLQDTYDKIVHNPLIIPE--GLNPRLRDLIEGLLCKDPNQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYLVFDLL------RKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKP
                                                                                                                                                   SNLLLGDDGHVKIADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWA
                                                                                                                                                                                 LNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQAAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --MEVPCDKP--FSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADF
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Pred. No. 1e-15;
58; Mismatches 115;
                                                                                                                                                                                                                                                                                                                           GVPDIKLHPWVTKNGEEPLPSE 420
                                                                                                                                                                                                                                                                                                                                                      345 TLKAVAEHPWIT--GEDGAISE 364
             178 FYMVLEYVDGKWAYDDSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%;
35.2%;
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A,Cross-references: SGD:S0003147
A,Map position: 7L
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                                                                                                                                                     279
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                      135
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Best Local 9
Matches 128
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R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
                  C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; phosphotransferase; protein kinase F;131-448/Domain: protein kinase homology <KIN>F;131-448/Domain: protein kinase ATP-binding motif
                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                             249
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                                                                                                                                                                                                                                                                                                  141 VVRLAYNESEDRHYAMKVLSK--KKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQ 198
                                                                                                                                                                                                                                                                                                                             303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 NPETRIGVPDIKCHPWVT-----KNGEEPLPS------EBEHCSVVEVTEGEV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IRKRSFGNPFEPQARREERSMSAPGNLLVKEG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine/threonine-protein kinase-like protein - Arabidopsis thaliana
NyAlternate names: protein T14D3.180
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Pate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                               --- LNOYKLOSEIGKGAYG
                                                                                                                                                                                                                                                         86 HISSSLAKTPITTSSFCSSGSSKNKVKETNRISLTYDPVSKRKVLNTYEIIKELGHGQHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGN
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A;Introns: 86/3; 111/3; 126/3; 151/3; 181/1; 222/3; 251/3; 312/3; 339/1
A;Note: T14D3.180
                                                                                                                                                                     Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                            Length 1142;
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llarity 37.0%; Pred. No. 4.4e-16;
Conservative 56; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                      EIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD
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                                                                                                                        Ouery Match
21.5%; Score 566; DB 2; L
Best Local Similarity 31.6%; Pred. No. 5.2e-18;
Matches 151; Conservative 82; Mismatches 135;
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A;Molecule type: DNA
A;Recidues: 1-382 <JOR>
A;Cross-references: EMBL:ALl38649
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Best Local Similarity
Matches 119; Conserv
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0y 293 DEGUSNOPEGNDAGLSSTAGTDARFAADE-ALSDSGOSFSG 331 0b 466 DEGUSTGRENERDEEDEPUSESBARDP-NNLEHAKVOTFAFFARELCTTOTTOBREG 524 0c 332	
Db 209 GVAMSTATGSTNIQSSHEQLLKSRALGTPAFFAPELCSTEKESCSSAIDIWSLGVTIYC 268 Qy 346 FVYGKCPFIDDFILALHRYIKNEPVYFPEEPELSEELKDLIKALDKN 393 :: :	17.8% Score 468 DB 2; Length 1246 Best Local Similarity 21.5% Pred. No. 1.1e-13 Best Local Similarity 21.5% Pred. No. 1.1e-13 Matches

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A;Cross-references: GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology «KIN»
F;25-33/Region: protein kinase ATP-bindding motif
F;48,65/142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable serine/threonine protein kinase (EC 2.7.1.-) SNFL3 - sorghum
N.Alternate names: SNF1 protein kinase homolog SNFL3
C,Species: Sorghum bicolor (sorghum)
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C,Accession: T14822
R,Annen, F.; Stockhaus, J.
Bot. Acta 111, 137-142, 1998
A,Fitle: SNFL3 a protein kinase homolog of Sorghum bicolor with a high similarity to the A,Fitler: preliminary; translated from GB/EMBL/DDBJ
A,Gatus: preliminary; translated from GB/EMBL/DDBJ
A,Robecule type: mRNA
A,Robecule type: mRNA
A,Residues: 1-461 < ANN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C;Keywords: phosphotransferase; protein kinase
F;10-266/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KNWEMEEKVRREIKILRLFMHPHIIRLYEVVETPSD--IYVVMEYVKSGELFDYIVE 110
                                                                                                                                                                                                                                                                                                                                                                          125 INQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFEGN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 HF-LKTSCGSPNYAAPEVI--SGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFK 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 DAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 GSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGP
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                                                                                                                                                                                                                                                                          DB 1; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 461;
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A;Experimental source: cultivar TX 430
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          16 LRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKI
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llarity 29.4%; Pred. No. 1.4e-12;
Conservative 73; Mismatches 135;
                                                                                                                                                                                                                                                                                                ; Pred. No. 1.2e-12;
64; Mismatches 94
                                                                                                                                                                                                                                                                        16.6%; Score 436.5; 33.7%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                             Similarity 33.7. 96; Conservative
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Best Local S:
Matches 96
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Best Local E
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Serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::|| | ::||| | :|| | :|| | 104 NHGRMREDEARRYFQQLINAVDYCHSRGVYHRDLKPENILLLDSYGNLKVSDFGLSALSQQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 QLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME-VP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KMVEQIKREISIMKLIKHPNVVRIYEVMG--SKTKIYIVLEFATGGELFORIV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNILLGDDGHVKIADFGVS--NQF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SMSAGLNLGNLF 329
                                                                                                                          probable serine/threonine kinase (EC 2.7.1.-) SNFL1 - sorghum NyAlternate names: SNFI protein kinase homolog SNFL1 (Species: Sorghum bicolor (sorghum) C;Species: Sorghum bicolor (sorghum) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: 114735 R;Annen, F.; Stockhaus, J. Plant Mol. Biol. 36, 529-539, 1998 A;Title: Characterization of a Sorghum bicolor gene family encoding putative ] A;Reference number: Z18177; MUID:98145442; PMID:9484448
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-440 <ANN>
A;Cross-references: EMBL:Y12464; NID:g2632251; PIDN:CAA73067.1; PID:g2632252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: SNFL1
C,Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases, protei
C,Keywords: phosphotransferase; serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.6%; Score 437; DB 2; Length 440; 29.7%; Pred. No. 1e-12; ive 72; Mismatches 136; Indels
DSEQEFKRETRFTSKCPPKEIVRKIEEAAKPLGFGVQKKNYKL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tase of Saccharomyces cerevisiae.

A;Reference number: A56009; MUID:94217693; PMID:8164654

A;Accession: A56009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: cultivar TX 430 C, Genetics:
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Best Local Similarity 29.74
Matches 114; Conservative
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A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
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completed: July 12, 2004, 04:54:05
R;LeGuen, L.; Thomas, M.
Gene 120, 249-254, 1992
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Job time : 59 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C; Superfamily: AMP-activated protein kinase; protein kinase homology C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine/threonine-specific protein kinase (BC 2.7.1.-) AK21 - Arabidopsis thaliana N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 11-Jun-1999
C;Accession: JC1446; S58266; S66334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NGEEPLPSEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRK 456
                                                                                                                                                                                              214
                                                                                             --- 411
                   NOFEG--NDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFID 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
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A;Cross-references: EMBL:U83797; NID:g1935915; PIDN:AAB52224.1; PID:g1935916
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                               probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potatc NyAlternate names: StubSNF1 protein
C.Species: Solanum tuberosum (potato)
C.Species: Solanum tuberosum (potato)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jan-2000
                                       GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 INOYKLOSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG
                                                                                             DFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 KIKGGYITLPS--HLSAGARDLIPRMLIVDPWKRMTIPBIRLHPW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 KIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPW 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T07788
R;Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A;Reference number: Z16133
                                                                                                                                                                                                                                                  457 RSFGNPFEPQ-ARREER 472
                                                                                                                                                                                                                                                                                    FDLSNLFEEKYGRREER 342
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Matches 96; Conserv
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C; Function:
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A; Accession: S66334
A; Molecule type: DNA
A; Cross-treferences: EMBL:X86966; NID:9928910
C; Comment: This enzyme plays an important role in a signal transduction cascade regulatify
C; Comment: This enzyme plays an important role in a signal transduction cascade regulatify
C; Comment: This enzyme plays an important role in a signal transduction cascade regulatify
C; Comment: This enzyme plays an important role in a signal transduction cascade regulatify
C; Function:
A; Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C; Function:
A; May-activated protein kinase; serine-phosphate or peptidyl-threonine
C; Superfamily: AMP-activated protein kinase; serine/threonine-specific protein kinase
F; I7-271/Domain: protein kinase ATP-binding motif
F; I7-271/Domain: protein kinase ATP-binding motif
F; Molecule type: Molecule Site: Lys, Glu, Asp, Lys #status predicted
F; 147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                            A,Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein A,Reference number: JC1446; MUID:93013041; PMID:1339373
                                                                                                                                                                           A, Accession: JC1446
A, Molecule type: DNA
A, Molecule type: Lost of the Library, May 1995
A, Description: Differential accumulation of the transcripts of 22 novel protein kinase A, Reference number: S58256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 144-198 CTHU>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
A;Thuemmler, F; Kirchner, M; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes
A;Reference number: S66314; MUID:96123233; PMID:8534852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 DAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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34.0%; Pred. No. 3.3e-12;
tive 59; Mismatches 98
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Best Local Similarity 34.0
Matches 97, Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 12, 2004, 01:20:58; Search time 53 Seconds (without alignments) 496.140 Million cell updates/sec Run on:

US-10-690-617-2 2634 1 MEGGPAVCCQDPRAELVERV......FGEGGKSPELPGVQEDEAAS 505

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P50526 schizosacch					Q38997 arabidopsis	Q9jlm8 mus musculu	xenobns	Q00372 candida gla	P06782 saccharomyc			rattı	O15075 homo sapien	xenol		-		Q91820 xenopus lae		rattu	homo	pomod		_	_	_	sacch	homo	7 homo	275 rattı	5831 hom	Q05512 mus musculu
ΙD	SSP1 SCHPO	PAK1 YEAST	KGS9 YEAST	SNF1 CANAL	SNF1 CANTR	KI10 ARATH	DCK1 MOUSE	ST6L XENLA	SNF1 CANGA	SNF1 YEAST	SNF1_SCHPO	GIN4 YEAST	DCK1 RAT	DCK1 HUMAN	STKB_XENLA	KMLC DICDI	KAPC_DICDI	KCCG HUMAN	STK6 XENLA	AAK2_RAT	KCCG_RAT	AAK2 HUMAN	ARK5 HUMAN	KIII HUMAN	LOK DROME	KCCG MOUSE	KCCD RAT	KCC4 YEAST	KCCA HUMAN	CHK2 HUMAN	KCCA RAT	STKB HUMAN	MRK2_MOUSE
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Length	652	1142	260	620	619	535	756	408	611	633	576	1142	433	740	432	295	648	472	407	552	527	552	199	794	476	529	533	1037	478	543	478	433	774
Query Match Length	23.5	21.5	19.3	16.6	16.4	16.2	15.7	15.6	15.5	15.3	15.3	15.3	15.3	15.2	15.1	15.0	15.0	14.9	14.8	14.8	14.8	14.7	14.7	14.7	14.7	14.6	14.6	14.6	14.6	14.6	14.6	14.5	14.5
Score	620	995	507.5	437	432	426.5	412.5	410	407	403.5	403	403	402.5	401.5	397	396	394	393	390.5	389.5	389	387.5	387	387	386	385.5	384.5	384.5	384	384		383	CD.
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P11798 mus musculu Q1357 homo sapien Q09170 schizosacch Q1354 homo sapien P21137 caenorhabdi P28652 mus musculu P05132 mus musculu P31751 homo sapien Q13131 homo sapien Q42626 neurospora P22987 schizosacch
KCCA MOUSE KCCD HUMAN CDS1_SCHPO KCCB_HUMAN KAPC CAREL KCCB_MOUSE AKT2_HUMAN KAPA HUMAN AAK1_HUMAN AKAY HUMAN
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4478 4499 4404 4404 4400 4400 4400 4400 440
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## ALIGNMENTS

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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 VEPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEP----LPSEERHCSV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GRLR-RKLGKLFRFRRPKARVFDSSSSVPSDSSIC 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 GKVKLGRDTVTRELLAIKIIPKTE------RPP-----KLGRANASSQKEKVRRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILGLEYLHCOKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGNDAQLSSTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |:| || :|| ::| | :|| || 371 NIPSTPDIGEEGRDILKRILCKDPEQRITIVEVKLHPWTLDGLKDPEKWLQNTDPSTVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; Score 620; DB 1; Length 652; 34.4%; Pred. No. 4.5e-33; ive 67; Mismatches 176; Indels '
                                                                                                                                                                                                                                                                           InterPro; IRR002290; Ser thr pkinase.
Promos, PR00069; pkinase; I.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00200; Frkc; I.
PROSITE; PS001007; PROTEIN KINASE ATP; 1.
PROSITE; PS001108; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 SVIPGSTSRLLPARPSLSARKLSLQER--PAGSYLEAQAGPYATG---
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W, B1931E5EB75A85DA CRC64;
                                                                                                                                                     EMBL, D45882; BAA08301.1; -. BYBL, AL049609; CAA40783.1; -. PYR, S58666; S58666. HSSP, Q53450; 1A06. GeneDB SPombe; SPCZ297.03; -. InterPro; IPR000719; Prot kinase. InterPro; IPR000219; Ser thr pkin AS. InterPro; IPR002299; Ser thr pkinase.
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Best Local Similarity
Matches 168; Conserv
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                                                                                                                                                                                                                                                                                                                                     Ξ
                                                                                                                                                                                                                                                     MEDLINE=97313264; PubMed=9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Aviles B. Maraujo R., Aviles B. Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakhara K., Namath A., Norgren R., Oefner P., Smith V., Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
Withen nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 256:45-53(1997).
-!- FUNCTION: May function by modifying and partially stabilizing thermolabile DNA polymerases, perhaps during DNA repair.
-!- PTM: Autophosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                               Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hovland P.G., Tecklenberg M., Sclafani R.A.;
"Overexpression of the protein kinase Pakl suppresses yeast DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD; S0000931; PAX1.
GO; GO:0004672; F:protein kinase activity; IDA.
GO; GO:0006468; F:protein maino acid phosphorylation; IGI.
GO; GO:0006468; P:protein maino acid phosphorylation; IDA.
InterPro; IPR000319; Prot kinase.
InterPro; IPR002290; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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ATP (BY SIMILARITY).
BY SIMILARITY.
Q -> H (IN REF. 2).
EVL -> DS (IN REF. 2).
EYL -> DS (IN REF. 2).
                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces
                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Serinc-threonine-protein kinase PAKI (EC 2.7.1.-).
PAKI OR YER129W OR SYGP-ORF45.
1142 AA
                                                                                                                           Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U18916; AAC03227.1; -.
EMBL; U13396; AAC4840.1; ALT_TERM.
PIR; S50632; S50632.
GermOnline; 139208; -.
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STANDARD;
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Mol. Gen. Genet. 256:4
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
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1142 AA;
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DB 1; Length 1142;

Score 566;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                      14;
                                                   140
                                                                                                                                                                                                                                                                                       304 DA----QLSSTAGTPAFMAPE-AISDSG-----QSFSGKA----LDVWATGVTLYC 345
                                                                                                                                                                                                                                                                                                      ---EELKDLILKMLDK 392
                                                                      | | | | : | | | : | : | : | HISSSLAKTPITITSSFCSSGSKNKVVKETNRISLIYDPVSKRKVLNIYEIIKELGHGQHG 145
                                                                                                             141 VVRLAYNESEDRHYAMKVLSK--KKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQ 198
                                                                                                                             EIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD------KPFSE 249
                                                                                                                                                                                                                              250 EQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGN 303
                                                                                                                                                                                                                                              ----EEEHCSVVEVTEGEV 434
                                                                                                                                                                                                                                                                                                                                                                                                                       192 EIAIMKKCHHKHVVQLIEVLÖÖLKSRKIYLVLEYCSRGEVKWCPPÖCMESDAKGPSLLŠF 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNSVRLIPSWTTVILVKSM-----LRKRSFGNPFEPQARREERSMSAPGNLLVKEG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95397594; PubMed=7668046; Coglievana M., Baruschi C.V.; Coglievana M., Bartani I., Klima R., Zaccaria P., Bruschi C.V.; The DNA sequence of a 7941 bp fragment of the left arm of chromosome VII of Saccharomyces cerevisiae contains four open reading frames including the multicopy suppressor gene of the pop2 mutation and a putative serine/threonine protein kinase gene.";
                                                   ----LNQYKLQSEIGKGAYG
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                        Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Probable serine/threonine-protein kinase YGL179C (EC 2.7.1.-).
         Pred. No. 3e-29;
; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                               346 FVYGKCPFIDDFILALHRKIKNEPVVFPEEPEIS----
                                                     HISPRAWRRPTIESHHVAISDAEDCVQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                                                        393 NPETRIGVPDIKLHPWVT-----KNGEEPLPS-
31.6%; Fig. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X83690; CAA58659.1; -.
EMBL; Z72701; CAA96891.1; -.
PIR; S57252; S57252.
HSSP; Q00534; IBI8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c / FY1679;
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGL179C OR G1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGS9 YEAST
P43637;
                         151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
                                                     98
          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGS9 YEAST
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89 GYSLOLKVENPRVNQEIEVMKRCHHENVVELYEILNDPESTKVYLVLEYCSRGPVKMCPE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 PDKRIKLADIKVHPFMCHYGKSDAASVLTNLETFHELKVSPPSSCKRVELVSLPVNSSFA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GV-----SNOFEGNDAQL--SSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 FVYGKCPFIDDFILALHRKIKNEPVVFPEEPEISE-------ELKDLILKMLDKN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 GPAKQL-LPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --MEVPCDKP--FSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 PETRIGVPDIXLHPWVTKNGEEPLPS-----EEEH------CSVVEVTEGEVKNSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 LLFGKLPFNANSGLELFDSIINKPLEFPSYEEMLNGATSGITMEEYTDAKDLLKKLLQKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
SGD; S0003147; TOS3.
InterPro: IPR000719; Prot kinase.
InterPro: IPR000217; Ser thr pkin AS.
InterPro: IPR002290; Ser thr pkin AS.
InterPro: IPR002290; Ser thr pkinase.
Pfam; PF000069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DoM; 1.
Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 32354 / B-311;
MEDLINE=98053924; PubMed=9393775;
MEDLINE=98053924; PubMed=9393775;
Petter R., Chang Y.C., Kwon-Chung K.J.;
"A gene homologous to Saccharomyces cerevisiae SNF1 appears to be essential for the viablilty of Candida albicans.";
Infect. Immun. 65:4909-4917(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----FEKR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y SIMILARITY.
EFFA0CSED58B5466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%; Score 507.5; DB 1; 35.2%; Pred. No. 7.8e-26; tive 58; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNF1_CANAL STANDARD; PRT; 620 AA. P52497; 000309; 01-0CT-1996 (Rel. 34, Created) 10-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Carbon catabolite derepressing protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344
64
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
56
79
189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 LIPS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 SLDS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NP BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                    VTKNGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQAR 468
                                                  318 LSKNKNSKIDVDEDVIRALSVTMGYDRDC-----KIVNVIEKANKQVAAGNSSSQQSK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 QLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQ 183
                                                                                                                   371 SSNEILDA--YLLMKENHALVKDLKKSKSENIESFLSQSPPPSPFPNRGSTSSAPGVQQ 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 RIGRYQIIKTLGEGSFGKVKLAQHVGTGQKVALKIINRKTLAK-----SDMQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                "Genetic evaluation of the function of SNF1 in Candida tropicalis.";
"Genetic evaluation of the function of SNF1 in Candida tropicalis.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Essential for release from glucose repression. It
interacts and has functional relationship to the regulatory
protein SNF4. Could phosphorylates CAT8 (By similarity).
-!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                     15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.4%; Score 432; DB 1; Length 619; larity 28.4%; Pred. No. 7.3e-21; Conservative 80; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; I.

ProDom; PD000001; Prot kinase; I.

PROSITE; PS00120; S TKC; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS500109; PROTEIN KINASE ST; I.

PROSITE; PS50011; PROTEIN KINASE DOM; I.

Transferase; Serine (threonine-protein kinase; ATP-binding; Phosphorylation; Carbohydrate metabolism; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-) () 0 OFCF1FC3DCE706D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                        619 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000119; Prot kinase.
InterPro; IPR008271; Ser Thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB024535; BAA75889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 E
70323 MW;
                                                                                      469 REERSMSAPGNLLVKEG-
                                                                                                                                                                                                                                                                                                                   Candida tropicalis (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
81
174
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q63450; 1A06
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfamily.
                                                                                                                                                                                                      CANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119;
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MOD_RES
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NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                    094168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                     RESULT 5
SNF1_CANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 QLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-----RVEREISYLRLLRHPHIIKLYDVI--KSKDEIIMVIEFAGKELFDYIVQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 FKKİSNGVYTLPN--YLSAGAKHLLTRMLVVNPLNRİTIHEIMEDDWFKQDMPDYLLPPD 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                similarity).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 DKPFSEEQARLYLRDVILGLEYLHCOKIVHRDIKPSNLLLGDDGHVKIADFGVSN-QFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDAQLSSTAGTPAFM-APEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                             STRAIN-ATCC 32354 / B-311;
Petter R., Kwon-Chung K.J.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Essential for release from glucose repression. It interacts and has functional relationship to the regulatory protein SNF4. Could phosphorylates CAT8 (By similarity).
-!- SUBCELLUIAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQ -> AR (IN REF. 2),
AGPEVDV -> SSVQKLMI (IN REF. 2).
YVMLCGRLPFDDEF -> GMSCCVVDXHSWTSS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                     82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 437; DB 1; Length 620; 29.1%; Pred. No. 3.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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A -> R (IN REF. 2).
R -> A (IN REF. 2).
S -> L (IN REF. 2).
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Interpro; IPR008271; Ser thr pkin AS.
Interpro; IPR002290; Ser thr pkinase.
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[2]
SEQUENCE OF 7-620 FROM N.A.
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les 122; Conserv
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Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Delseny W., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Nancker P., Catcolico L., Weissenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
Niedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Niedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
R. Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionari B.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Ararro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
A Haarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argiricu A., Flores M., Liguori R., Vitale D.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujil C.Y., Shea T.P.,
                                                                 | | : | : | : | : | : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 KKISNGVYILPN--YLSPGAKHLLTRMLVVNPLNRITIHEIMEDEWFKQDMPDYLLPPDL 316
                                                                                                                                                                                                                          244 DKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSN-QFEG 302
                                                                                                                                                                                                                                                                                                                               143 RGKMPEDEARRFFQQIIAAVEYCHRHKIVHRDLKPENLLLDDQLNVKIADFGLSNIMTDG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 RKIKNBPVVFPEEPEISEELKDLILKMLDKNPETRIGV-------PDIKLHPWV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 TKNGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARR 469
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GGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPC 243
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93013041; PubMed=1339373; He Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.; le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.; Structure and expression of a gene from Arabidopsis thaliana encoding a protein related to SNF1 protein kinase."; dene 120:249-254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Lessard P., Kreis M., Thomas M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIIO ARATH STANDARD; PRT; 535 AA.
038997; 004728; 039076; QBRWD2;
15-JUL-1999 (Rel. 38, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10)
KIN10 OR SKIN10 OR AT3601090 OR T4P13.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
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MEDLINE=21016720; PubMed=11130713;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE Columbia;

MEDLINE=22954860; PubMed=14593172;

MEDLINE=22954860; PubMed=14593172;

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Lakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldemith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.M., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakirai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=Q38997-2; Sequence=VSP 009001; TISSUE SPECIFICITY: Expressed in roots, shoots and leaves. SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOI, Gen. Genet. 245:390-396(1994).
-!- FUNCTION: May play an important role in a signal transduction
cascade regulating gene expression and carbohydrate metabolism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       le Guen L., Thomas M., Kreis M.; "Gene density and organization in a small region of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [sold=038997-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR000719, Prot kinase.
InterPro, IPR008271; Ser_thr_pkin_AS.
InterPro, IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, Q63450; 1A06.
InterPro; IPR001772; Kinase Cterm.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=95115691; PubMed=7816049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY093170; AAM13169.1; -. BT010386; AAQ56829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M93023; AAA32736.1; -.
EMBL; X79707; CAA56146.1; -.
EMBL; AC008261; AAF26165.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X94757; CAA64384.1;
PIR; JC1446; JC1446.
                                                                                                                                                                                                                                   Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         higher plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1;
                                                                                                                                                                                                              thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qenome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
EMBL;
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361 LHRKIKNEPVVFPEE--PEISEELKOLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 LFDQILMGQVDFPSPYWDNVSDSAKELINMMLLVNVDQRFSAVQVLEHPWVNDDG---LP 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

3DIDBF18C23129F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 412.5; DB 1;
; Pred. No. 1.8e-19;
71; Mismatches 199;
                                                  subfamily.
SIMILARITY: Contains 2 doublecortin domains.
                                                                                                                                                                                                                                                                                                                                                                                    DOUBLECORTIN 1.
DOUBLECORTIN 2.
SER/PRO-RICH.
PROTEIN KINASE.
                                                                                                                                                                                  HSSP, 063450, 1A06.

MGD: MGI:1330661; Dcamkl.

InterPro; IPR000353; DCX.

InterPro; IPR00019; Prot kinase.

InterPro; IPR00220; Ser_thr_pkin_AS.

InterPro; IPR00220; Ser_thr_pkin_ase.

Pfam; PF03607; DCX, 2.

Pfam; PF03607; DCX, 2.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00520; STKC; 1.

PROSITE; PS50309; DC; 2.
                                                                                                                                                                           EMBL; AF155819; AAF26673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%;
27.6%;
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269
358
663
420
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756 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    57
186
298
406
412
435
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Best Local Simil
Matches 140; C
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ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
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                                                                                                                                                                                                                                                                                                                                                                                   GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGFVMEVPCD 244
                                                                                                                                                                                                                                                                                                                                                                                                                              245 K-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFEGN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 194 HF-LKTSCGSPNYAAPEVI--SGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFK 250
                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                       BY SIMILARITY.

ATP (BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

Missing (in isoform 2).

/FIId=VSP_009001.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine-threonine-protein kinase DCAMKLI (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Neurosci. Res. 58:567-575(1999).
-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20004649; PubMed=10533048;
Burgess H.A., Martinez S., Reiner O.;
"KIAA0369, doublecortin-like kinase, is expressed during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPW 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                        Score 426.5; DB 1; Length
Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                 98; Indels
                                                                                                                                                                                                                                                                                                                                                   FFFC383223FD8317 CRC64;
                                                                                                                                                             Phosphorylation; Alternative splicing.

ODMAIN 42 294 PROTEIN KINASE.
NP BIND 48 56 THE (BY SIMILARITY).

OOMAIN 315 355 UBA.
                                                                                                                                                                                                                                                                                                              59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756 AA.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00149; UBA_domain.
Pfam; PF00169; Pkinase; 1.
Pfam; PF00627; UBA, 1.
PRINTS; PR00109; TYRKINASE.
PRODOW, PR00109; TYRKINASE.
SWART; SW00120; S TKC; 1.
SWART; SW00165; UBA; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                  61181 MW;
                                                                                                                                                                                                                                                                                          16.2%;
                                                                                                                                                                                                                                                                                                     34.0%;
                                                                                                                                                                                                                                                                                                              97; Conservative
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165
71
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                                                                                                                                                                                                                                                                   535 AA;
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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198
1
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                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                        ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                   185
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                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                 RES
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DCK1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 RPAGSYLEAQAGPYATGPAS----HISPRAWRRPTIESHHVAISDAEDCVQL----NQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAQGGPA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 KQLLPLERVYQEIAILKKLDHVNVYKLIEVLDDPAEDNLYLVFDLLRKGPVMB-VPCDKP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 NDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF--IDDFILA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---PLYTVCGTPTYVAPEIIAETGY---GLKVDIWAAGVITYILLCGFPPFRGSGDDQEV 612
                                                                                                SISIEM (By BIMILATILY).
SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PPRARAASVIPGSTSRLLPARPSL-SARKLSLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGD--DG--HVKIADFGVSNQFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
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SEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPG 478
                                            570 ENEHQLSVA----GKIKKHFNTGPKPSSTAAGVSVIATTALDK--ERQVFRRRRNQD--- 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinse family.";
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYITC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBCELLUIAR LOCATION: Localizes to the spindle pole during mitosis especially from prophase through anaphase. Partially colocalised with gamma tubulin in the centrosome, from S to M phase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roghi C., Le Guellec R., Paris J., Couturier A., Philippe M.;
"Eg2, selected by differential screening encodes a new Xenopus protein
kinase family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle; Transferase; Serine/Threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Serine,threomine protein kinase Eg2-like (EC 2.7.1.37) (p46XlEg22).

Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Phosphorylated (By similarity).
SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
Aurora subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 410; DB 1; Length 408; 29.9%; Pred. No. 1.2e-19; Live 61; Mismatches 155; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
97F6A69C7357AEE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                     408 AA
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                                                                                                                                                                                 ---VRSRYKAQPAPPELNSESEDYSPS 744
                                                                                                                    479 NLLVKEGFGEGGKSPELPGVQEDEAAS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, Z17206; CAA78914.1; ALT_INIT.
HSSP; P24941; 1AQ1.
InterPro; IPR000713; Prot kinase.
InterPro; IPR000871; Ser_thr_pkin_AS.
InterPro; IPR001291; Ser_thr_pkinase.
InterPro; IPR001295; Tyr_pkinase.
Ffam; PF00066; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S TKC; 1.
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                                                                                                                                                                                                                                                                                                                                     STANDARD;
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154
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263
408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Egg;
                                                                                                                                                                                                                                                                                                                                  STGL XENLA
091819;
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STGL_XENIA
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DT 28-FEB
DT 28
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88

80;

37 PTRNGVDPPPRARAASVIPG-STSRLL----PARPSLSARK--LSLQERPAGSYLEAQA

Conservative

Local Similarity

3est Local Sim Matches 126;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          300 FEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFIL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PATHGHQTSKPQGPNENRNPQQTSHSSTPNMEKKGSTDQGKTLAVPKEEGKKKQ 134
                                                                                                                                                                                                                                                 181 AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVM- 239
24 PKRIPVSQPPSTQVRPPVTGVSAQRILGPSNVPQRVMMQAQKPVLSNQKPTAQGLLR--- 80
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SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                       GPYATGPASH-----ISPRAWRRPTIESHH--------VAISDAED---
                                                                                                                                                                                                                                                                                                                                      240 EVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQ
                                                                                                                                                                                                                                                                                                                                                            286 VHAPSSRRTTLCGTLDYLPPEMI--EGRMHDEK-VDLWSLGVLCYEFLVGKPPFETDTHQ
                                                                                                                                                         122 - CVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ
                                                                                                                                                                                                                                                                                          176 LEKAGVEHQL-----RREVEIQSHLRHPNILRLYGYFHDAS--RVYLILDYAPGGELFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 ALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97101049; PubMed=8945576;
Petter R., Kwon-Chung K.J.;
"Disruption of the SNF1 gene abolishes trehalose utilization in the
pathogenic yeast Candida glabrata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 64:5269-5273(1996).
-!- FUNCTION: Essential for release from glucose repression. It interacts and has functional relationship to the regulatory protein SNF4. Could phosphorylates CATS (By similarity).
-!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                     (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-UU1-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 AA.
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InterPro; IPR008271; Ser_thr_pkin_AS.
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DE 402
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233:1175-1180(1986)
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633 AA;
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Best Local Similarity
Matches 121; Conserv
                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SDMQG------RIDREISYLRILRHPHIIKLYDVI--KSKDEIIMVIEYAGN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                               77
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EIRNAYILIKDNKSLIKDMKQDNNVTQELDTFLSQSPPTFQQNGDGMKASEDQKKKHSGR
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-) (BY SIMILARITY) 89E17812A4900CD0 CRC64;
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MEDLINE=86289463; PubMed=3526554;
Celenza J.L., Carlson M.;
Talay yeast gene that is essential for release from glucose repression encodes a protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.1e-19;
0; Mismatches 135; Indels 120;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
SNF1 OR CAT1 OR CRI OR PAS14 OR GLC2 OR YDR477W OR D8035.20.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                               15.5%; Score 407; DB 1; Length 611; 26.2%; Pred. No. 3.1e-19;
Production, irravozdy; Ser_thr_pkinase.
Production: Profologe; pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMOSITE; PSCOLOG; PROTEIN KINASE AFP; 1.
PROSITE; PSCOLOG; PROTEIN_KINASE_ST; 1.
PROSITE; PSCOLOG; PROTEIN_KINASE_DOM; 1.
TRANSferase; Serine/threonine-profein kinase; ATP-binding; Phosphorylation; Carbohydrate metabolism; Nuclear protein.
DOMAIN
6 17
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ATP (BY SIMILARITY)
ATP (BY SIMILARITY).
BY SIMILARITY.
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ACT SITE
MOD RES
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No. 12 Posterior R. A. Maligan J., Allen E., Araujo R., Aviles E., Man B. Bertzch F.S., Maligan J., Allen E., Araujo R., Aviles E., Duncan M., Berroch F.S., Maligan J., Cheff S., Cherry J. M., Change E. Duncan M., Readala Carl, Makahayamar. M. Cancer P. D. Carl B. Duncan M., Readala Carl, Makahayamar. M. Cancer D. Carl B. Duncan M. Readala Carl Makahayamar. M. Carl Carl B. Duncan M. Readala Carl M. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogren T. Shogr
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RX MEDLINE=2184901; PubMed=11859360;

RX MEDLINE=21849401; PubMed=11859360;

RA WOOd V. Gwilliam R. Rajandream M.A., Lyne M., Lyne R., Stewart A., RA WOOd V. Gwilliam R., Rajandream M.A., Lavis P. D. Bowman S., A Sgource J., Peat N., Hayles J., Davis P., Feltwell T., Fraser A., Collins M., Connor R., Croin A., Davis P., Feltwell T., Fraser A., Reditles S., Goble A., Hamlin N., Harris D., Hudalgo J., Hodgen G., A Jense K., Jones L., Jones M., Leather S., McDonald S., McLean J., Ander M., Leather S., McDonald S., McLean J., Ander R., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Ramoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A Jones K., Saunders D., Sammonde M., Squares S., Stevens K., Sharp S., Relton J., Simmonde M., Squares R., Squares S., Stevens K., Rabinowitsch B., Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Rudodavaf U., Volckaert G., Aert R., Robben J., Grymonprez B., Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Rudeties I., Reck A., Lehrach H., Reinhardt R., Pohl T.M., Beer P., Zimmermann W., Wedler H., Nambutt R., Purnelle B., Rager P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., A Golfeau A., Cadieu B., Dreano S., Hunt C., Moore K., Hurst S. M., A Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Rabaga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bomito J., L., Moreno S., Armstrong J., Forsburg S.L.,
SDAEDCVQINQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPP 176
                                                                                                        229
                                                                                                                               230 - FDLLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGH 288
                                                                                                                                                                                                                                VKIADFGVSN-QFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFV 347
                                                                                                                                                                                                                                                                                                                             348 YGKCPFIDDFILALHRKIKNEPVVFPEEPRISEELKDLILKMLDKNPETRIGV------ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 CRRLPFDDESIPVLFKNISNGVYTLPK--FLSPGAAGLIKRMLIVNPLNRISIHEIMQDD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 WFKVDLPEYLLPPDLKPHPEEENENNDSKKDGSSPONDEIDDNLVNILSSTMGYEKDEIY 364
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                                                                                                177 RGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLV----
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                            SVVEVTE----GEVKNSVRLIPSWTTVILVKSMLRKRSFGN----
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Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) SNF1-like protein kinase (EC 2.7.1.-).
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                                                                                                                                               94 ---SDMQG-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- VVEV----TEGEVKNSVRLIPSWTTVILVKS 452
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                                                                             Nature 415:871-880(2002).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 INQYKLOSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQAAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYL-----VFDLLRKGPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 MEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Serine/threonine-protein kinase; ATP-binding.
DOMAIN 34 285 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.5%; Pred. No. 5.2e-19; ive 70; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
BY SIMILARITY.
E5857E8F171E7B50 CRC64;
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Pot:
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UBA.
ATP (BY SIMILARITY)
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HSSP; Q63450; 1A06.
GeneDB Spoude; SPCC74.03c; ...
InterPro; IPR00871; Ser thr pkin AS.
InterPro; IPR00871; Ser thr pkin AS.
InterPro; IPR00871; Ser thr pkin AS.
InterPro; IPR00449; UBA domain.
Pfam; PF00069; pkinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS00108; PROTEIN KINASE DOM; I.
PROSITE; PS00108; PROTEIN KINASE DOM; I.
PROSITE; PS00108; PROTEIN KINASE ST; I.
                                                                                                                                      subfamily.
-!- SIMILARITY: Contains 1 UBA domain.
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Matches 111; Conservative
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                                                                                                                                                            Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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R PIR; S59359; S59359.

R HSSP; Q63450; 1A06

R Germonline; 140999; --

R GG; GO:0005935; CIbud neck; IDA.

GG; GO:00005935; Cibud neck; IDA.

GG; GO:0000921; P:septin checkpoint; IGI.

GG; GO:0000921; P:septin ring assembly; IGI.

R GG; GO:0000921; P:septin ring assembly; IGI.

R GG; GO:0000921; P:septin ring assembly; IGI.

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R InterPro; IPR002071; Ser thr pkin as.

R InterPro; IPR001245; Tyr pkin as.

R InterPro; IPR001245; Tyr pkin as.

R Pfan; PR00109; Tyr RKINASE.

R PROSITE; PR00109; Prot kinase; 1.

R PROSITE; PR00101; PROTEIN KINASE ATP; 1.

R PROSITE; PR00101; PROTEIN KINASE ATP; 1.

R PROSITE; PR00101; PROTEIN KINASE ATP; 1.

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                                                                                                                                                                                                                                                                   Longtine M.S., Fares H., Pringle J.R.; "Role of the yeast Gin4p protein kinase in septin assembly "Relationship between septin assembly and septin function." J. Cell Bool. 143:719-736(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129857 MW; EC16FF4BB49DD811 CRC64;
                                                               01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine-protein kinase GIN4 (EC 2.7.1.-).
GIN4 OR YDR507C OR D9719.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                PRT; 1142 AA.
                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                    MEDLINE=99030835; PubMed=9813093;
                                                    (Rel. 35, Created)
                  STANDARD;
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GIN4 YEAST
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                      GNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF--IDDFIL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TLLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPSIRDSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK-----N 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVIL-----VKSMLRKRSFGNPFE 464
                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A., Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T., Seger R., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.; "Hippocampal plasticity involves extensive gene induction and multiple callular mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
                                                                                                                                                                  STTPDALPYGIER---EIIIMKLLNHPNVLRLYDVWE--TNTDLYLVLEYAEKGELFNLL
                                                                                                                                                                                                                                                                                                                         ---NTGNVSGTSIVĠ
                                                                                                                    GPAKOLLP--LERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVP
                                                                                                                                                                                                                                                                       CDK-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Neurosci. 10:75-98(1998).
-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
36-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2000 (Rel. 39, Last annotation update)
11-MAY-2000 (Rel. 39, Last annotation update)
12-MAY-2000 (Rel. 39, Last annotation update)
13-MAY-2000 (Rel. 39, Last annotation update)
13-MAY-2000 (Rel. 39, Last annotation)
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13-MAY-2000 (Rel. 39, Last annotation)
13-MAY-2000 (Rel. 
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16 IGPWKLGETLGLGSTGKVQLARNGSTGQEAAVKVISKAVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Wistar;
MEDLINE=98364306; PubMed=9699150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U78857; AAC99476.1; -.
HSSP; Q63450; 1A06.
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DCAMKL1 OR CPG16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POARREE 471
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Gaps

48;

Conservative

Best Local Similarity

Matches 119;

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406
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                                                                                                                                                                                                        127
                                                                                                                                                                                                                                              -----YKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPP 175
                                                                                                                                                                                                                                                                                      PRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHYNVVKLIEVLDDPAEDNLYLVFDLLRK 235
                                                                                                                                                                                                                                                                                                   236 GPVME-VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGD--DG--HVK 290
                                                                                                                                                                                                                                                                                                                                           291 IADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGK 350
                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 PWVNDDG---LPENEHQLSVA----GKIKKHFNTGPKPSSTAAGVSVIATTALDK--ERQ 388
                                                                                                                                                                                                                        GSQLSTPRSGKSPSP-SPTSPGSLRKQRISQHGGSSTSLSSTKVCSSMDENDGPGEEESD 70
                                                                                                                                                                                                                                                                 71 EGFQIPATITERYKVGRTIGDGNFAVVKECIERSTAREYALKIIKKSKC------
                                                                                                                                                                                                                                                                                                                                                                                 CPF--IDDFILALHRKIKNEPVVFPEE--PEISEELKDLILKMLDKNPETRIGVPDIKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                 278 PPFRGSGDDQEVLFDQILMGQVDFPSPYWDNVSDSAKELINMMLLVNVDQRFSAVQVLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWVIKNGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWITVILVKSMLRKRSFGNPFEPQ
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                    83;
                                                                                                                                                                                                      GSYLEAQAGPYATGPASHISPRAWRRPTIESH---HVAISDAEDCVQLNQ----
                                                                                                                                                               ; Score 402.5; DB 1; Length 433;
; Pred. No. 3.9e-19;
69; Mismatches 179; Indels 83
                                               PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                               SER/PRO-RICH (BY SIMILARITY)
                                                                                                                                 SIMILARITY.

OCESE06E152A557D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 VFRRRRNQDVRGRYKAQPA-----PPELNSESEDYSPS 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 ARREERSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS
                                                                                                            ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                         PROTEIN KINASE.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     740 AA.
        ProDom; PD000001; Prot_Kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS001007; PROTEIN KINASE ATP; 1.
PROSITE; PS010109; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                          433 AA; 47680 MW;
                                                                                                                                                               15.3%;
27.9%;
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                         Best Local Similarity 21.37
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                        340
394
97
112
204
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                                                                                                                                                                        Similarity
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                                                                     Neurogenesis.
DOMAIN
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015075;
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                                                                                                                                 ACT SITE
SEQUENCE
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NP BIND
BINDING
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                                                                                        DOMAIN
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DCK1_HUMAN
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Isold=015075-4; Sequence=VSP 004905, VSP 004905, TISOLG=015075-4; Sequence=VSP 004905, VSP ESSED IN BRAIN, DETECTABLE IN LUNG AND LUYER, BUT NOT IN KIDNEY. IN ADULT TISSUES, EXPRESSED UBIQUITOUSLY IN THE BRAIN, DETECTABLE IN THE HEART, LIVER, SPLEER, THENGS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE AND COLON. THE TYPE A ISOFORMS SEEM TO BE EXPRESSED PREDOMINANTLY IN FETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99162404; PubMed=10051403; Matsumoto N., Pilz D.T., Ledbetter D.H.; Matsumoto N., Pilz D.T., Ledbetter D.H.; Matsumoto N., Pilz D.T., Ledbetter D.H.; Genomic structure, chromosomal mapping, and expression pattern of human DCAMKL1 (KLAA0369), a homologue of DCX (KLIS)."; Genomics 56:179-183(1999).

-! FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING BENEROWAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
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SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;

Comment=Additional isoforms seem to exist. Type A (AS and AL)
and type B (BS and BL) isoforms differ respectively by the
presence or absence of the doublecortin domain. An alternative
splicing occurring in 3' of the mRNA produces the long (L)
instead of the short (S) isoforms;
                                                                                                                                                                                                                                                                                  MEDLINE=99156863; PubMed=10036192; Sossey-Alaoui K., Srivastava A.K.; MEDAMKL1, a brain-specific transmembrane protein on 13q12.3 that is similar to doublecortin (DCX)."; Genomics 56:121-126(1999).
sequences of unidentified human genes. VI 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE=98419166; PubMed=9747029;
CMODI Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y.,
Takhashi E.-I., Fujiwara T.;
"Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin.";
J. Hum. Genet. 43:169-177(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1; Synonyms=AS;
IsoId=O15075-2; Sequence=VSP_004907;
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IsoId=015075-1; Sequence=Displayed;
                                                                                                                                                                                                             5
"Prediction of the coding sequences
The complete sequences of 100 new cD
code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                 [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB002367; BAA20824.1; -.
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Genew; HGNC:2700; DCAMKL1.
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Conservative
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Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P24941; 1CKP
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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                                                                                                           XENLA
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NP_BIND
BINDING
ACT_SITE
MOD_RES
MOD_RES
MUTAGEN
SEQUENCE
               716
                                                                                        STKB_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 RSTTKSPG-----PSRRSKSPASTSSVNGTPGSQLSTPRSGKSPSP-SPTSPGSLRKQR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YKLOSEIGKGAYGVVR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 LAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQEIAIL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRYKHPNIVLLIEEMDVPTE--LYLVWELVKGGDLFDAITSTNKYTERDASGMLYNLASA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 SSQHGGSSTSLASTKVCSSMDENDGPGEEVSEEGFQIPATITERYKVGRTIGDGNFAVVK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSEEEHCSVVEVTEGEV 434
                                                                        R InterPro; 1rkvvvz., 2.-.

R Pfan, PPO3607; DCX; 2.

R Pfan, PPO3607; DCX; 2.

R ProDom; PD000001, Prot kinase; 1.

R SWART; SW00237; DCX; 2.

DR SWART; SW00230; DCX; 2.

DR PROSITE; PS50309; DC; 2.

DR PROSITE; PS60309; DC; 2.

DR PROSITE; PS60309; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ATP; 1.

RW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;

KW Neurogenesis; Alternative splicing.

FT DOMAIN S7 143 DOUBLECORTIN 1.

TOMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTALDKERQÜFRRRRNQDVRSRYKAQPAPPELNSESEDYSP
SSSETVRSPNSPF -> LDHGFTIKRSGSLDYYQQPGMYWI
RPPLLIRRGRFSDEDATRM (in isoform 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 RAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 KKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME-VPCDKPFSEEQARLYLRDVILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 LEYLHCQKIVHRDIKPSNLLLGD--DG--HVKIADFGVSNQFEGNDAQLSSTAGTPAFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNSVRLIP-----SWTTVILVKSMLRKRS-FGNPFEPQARREERSMSAPGNLLVKEGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEAISDSGOSFSGKALDVWATGVTLYCFVYGKCPF--IDDFILALHRKIKNEPVVFPEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in isoform 3 and isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
POLY-ARG.
Missing (in isoform 3 and isoform 4
//FIId=VSP 004905.
PASTSS -> MLELIE (in isoform 3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 401.5; DB 1; Length 740; 26.9%; Pred. No. 8.9e-19; ive 75; Mismatches 186; Indels 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0006468; P:protein amino acid phosphorylation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D7B6D855099A315C CRC64;
                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTId=VSP 004906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoform 3).
/FTId=VSP 004907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 IESH---HVAISDAEDCVQLNQ-----
                 InterPro; IPR003533; DCX.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser_thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                            ATP
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269
340
647
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Best Local Similarity
Matches 134; Conser
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390
396
419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Serine/threonine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY PKA) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MG(2+).
SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K->I: LOSS OF ACTIVITY.
T->A: LOSS OF AUTO-PHOSPHORYLATION.
F4D98A06C52560F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Prot_kinase.
InterPro; IPR000719; Ser_thr_pkina.AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00069; pkinase; I.
Swarp; Sm00202; STKG; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; I.
PROSITE; PS001107; PROTEIN_KINASE_ATP; I.
PROSITE; PS50011; PROTEIN_KINASE_DM; I.
PROSITE; PS50011; PROTEIN_KINASE_DM; I.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.8e-19;
46; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine-fibreonine protein kinase 11 (EC 2.7.1.37)
protein kinase XEEK1) (Egg and embryo kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION
                                                                                                                              432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 397;
                                                                                                                                                                                                                                                                            STK11 OR EEK1.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESIS.
                                                                                                                              PRT;
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MEDLINE=96278908; PubMed=8662877;
||| || : |
----PELNSESEDYSPS 728
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66
81
179
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58
81
179
192
427
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192
432 AA;
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Search completed: July 12, 2004, 04:51:13 Job time : 56 secs This Page Blank (uspto)

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July 12, 2004, 01:17:43; Search time 102 Seconds (without alignments) 1398.887 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human kin Human kin Human Pro Human Pro Human pro
Human Non
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Rat amino
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	_	_	Abr52943 Protein s	Abb78798 Serine/th	Abr40710 Zea mays	Aar40842 SHPP. 8/2	Aab03425 Wheat put	Abr40719 Triticum	Aab03419 Soybean p	Abr40713 Glycine m	Aab03421 Soybean p	Abr40715 Glycine m	Aab03423 Soybean p	Abr40717 Glycine m	Abb78797 Protein k	Abr44015 Human SNF	Aag70854 C albican	Aab03417 Corn puta	Abr40709 Zea mays
ABB66416	ABU11714	AAM25471	ABR52943	ABB78798	ABR40710	AAR40842	AAB03425	ABR40719	AAB03419	ABR40713	AAB03421	ABR40715	AAB03423	ABR40717	ABB78797	ABR44015	AAG70854	AAB03417	ABR40709
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881	648	611	266	526	452	436.5	430.5	430.5	429.5	429.5	428.5	428.5	428	428	427	426.5	426.5	424.5	424.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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(HK), that has homology to members of the calcium/calmodulin-dependent protein kinase kinase subfamily. The mechanism of action of the protein of the invention is that of a kinase modulator. The human kinase of the invention is useful for creating a pharmaceutical composition for treating a disease or condition mediated by the human kinase. HK is also useful to provide a target for diagnoshing a disease or predisposition to disease mediated by HK, and is also useful in pharmacogenic analysis. HK is useful for treating a disorder characterised by absence of anappropriate or unwanted expression of HK, also as an immunogen to raise antibodies by administering HK to a mammalian organism e.g. rat, rabbit or mouse. Nucleic acids of the invention are useful as hybridisation probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells expressing a native HK are useful for assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for present invention are assaying a native HK are useful for assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for present invention are expressed in humans in the eye (retinoblastomas) and brain. The current sequence represents the amino acid sequence of the human kinase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnosing
                                                                 /note= "wild-type Glu is replaced by Gly as a result of
an SNP (single nucleotide polymorphism) in the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated peptide designated human kinase
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|Jabel= protein_kinase_C_phosphorylation_site
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/label= ATP/GTP-binding_site_motif_A
/note= "P-loop"
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/note= "cAMP- and
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2000US-0247031P.
2000US-00729995.
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06-DEC-2000;
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AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
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                                                                                                                                                                                                                                                   EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
                                                                                                                                                                                                                                                                                                            Human; kinase polypeptide; PKIN-19; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
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LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                      LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
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2000US-0222112P.
2000US-0222831P.
2000US-0224729P.
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28-JUL-2000;
04-AUG-2000;
11-AUG-2000;
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Length 505;

100.0%; Score 2634; DB 5; 100.0%; Pred. No. 2.8e-236;

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Conservative

Matches 505; Query Match

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Local Similarity

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1 MEGGPAVCCQDPRARLVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR

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The present invention relates to an isolated human kinase polypeptide

(PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is

useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
lymphoma, melannoma), an immune disorder (e.g., acquired immunodeficiency
syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's

disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a

cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial

infarction), and a lipid disorder (e.g., fatty liver, cholestasis,

daucher's disease, Niemann-Pick's disease). PKIN is useful in a number of

drug screening techniques and to analyse the protecome of a tissue or cell

type. PKIN is useful for creating knockin humanised animals or transgenic

animals to model human diseases, in somatic or germline gene therapy, to

generate a transcript image of a tissue or cell type, for detecting

differences in the chromosomal location due to translocation, inversion,

cycle and apping naturally occurring genomic sequences. PKIN is useful

to probes for mapping naturally occurring genomic sequences. PKIN is useful

conthern or northern analysis, dot blot or other membrane-based

technologies, in PCR technologies, in dipstick, pin, multiformat enzyme

linked immunosorbent (ELISA)-like assays and in microarrays utilising

fluids or tissues from patients to detect altered PKIN expression. The
                                                                                                                                                                                                                                                                                                        New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.
                                                                        Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding
ott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 168-170; 196pp; English.
INCYTE GENOMICS INC.
                                                                                                                                                  Yao MG, Elliott VS, Recipor
Tang YT, Xu Y, Walsh RT,
                                                                                                                                                                                                                                   WPI; 2002-206083/26.
                                                                             Yue H,
                        THORNTON M.
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                                                                                                     Patterson C,
Tribouley CM,
                                                                             Chornton M,
                          (THOR/)
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Sequence 505 AA;

o; LHRKIKNEPVVFPEEPEISEELKOLILKOMLDKNPETRIGVPDIXLHPWVTKNGEEPLPSE 420 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120 120 121 DCVQLNQYKLQSBIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180 AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME 240 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300 EGNDAQLISSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360 121 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180 241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300 EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360 9 1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60 1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR Gaps 0, 99.7%; Score 2626; DB 5; Length 505; 99.8%; Pred. No. 1.6e-235; ive 0; Mismatches 1; Indels 0 Conservative Local Similarity nes 504; Conserv 181 241 301 361 Query Match Best Loca Matches 원 g g 8 셤 ઠે à g δ ð

crimination of the mucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that medulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of 361 LHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE 420 The invention discloses a composition comprising two or more isolated rat for EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal. Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. Costigan M; Human Protein NP_115670, SEQ ID NO 7868. LVKEGFGEGGKSPELPGVQEDEAAS 505 ADE61939 standard; protein; 505 AA. Befort K, Claim 1; Page; 1017pp; English. 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. L4-AUG-2002; 2002WO-US025765 (first entry) (GEHO ) GEN HOSPITAL CORP. WPI; 2003-268312/26. Woolf C, D'urso D, GENBANK; NP 115670. (FARB ) BAYER AG. WO2003016475-A2. 29-JAN-2004 Homo sapiens 27-FEB-2003. ADE61939; 481 ADE61939 ID ADE6 RESULT 3 Š g ò 셤

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the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                             Length 505;
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                                                                            Query Match 99.7%; Score 2626; DB 7;
Best Local Similarity 99.8%; Pred. No. 1.6e-235;
Matches 504; Conservative 0; Mismatches 1;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising ne nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a agent to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynpetides are method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the cativity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides or their antibodies. The polypucleotide or more complained by a pecification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more complained by a specification) which is differentially expressed during pain. Note: the specialication) which is differentially expressed during pain. Note: the specialication but was obtained in electronic form directly from WIPO at the polymous or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the compound or the sequence data for this patent did not form part of the printed or the compound or the compound or the compound or the compound or the compound or the com
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Les 504; Conservative
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                                                                                                                         Woolf C, D'urso D,
                                                                                                                                                                                                           WPI; 2003-268312/26
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                                                                                                                                                                                                                                                                                               Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; barkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunoadulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autonimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
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                                                       BEHCSUVEVITEEEVKNSVRLIPSWTTVILVKSMIRKRSFGNPFEPQARREERSMSAPGNL
              LHRKIKNEPVVPPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                       EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
Zhang J, Zhao QA, 1
2, Wang Z, Ghosh M;
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Yang Y, Ma.Y, Yamazaki V, Chen R,
F, Wang J, Wang D, Drmanac RT;
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                                                                                                              LVKEGFGEGGKSPELPGVQEDEAAS
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                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
                                                                                                                                                                                                                                                                                                             EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF1DDF1LA
                                                                                                                        MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                                                                                                                                                             78 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPRARAASVIPGSTSR
                                                                                                                                                                                                                                            138 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                                                                                                                                                                                                                                                                                                       AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 EEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
                                                                                   Gaps
                                                                                   ..
                                           Length 582;
                                                                                 Indels
                                                            8.9e-235;
                                                            Pred. No. 8.9e
0; Mismatches
                                           Score 2619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2001; 2001US-0274101P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-027432P.
09-MAR-2001; 2001US-0274469P.
12-MAR-2001; 2001US-02746469P.
13-MAR-2001; 2001US-027535P.
                                           99.4%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                             503; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV15b protein.
                                                            Similarity
Sequence 582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200272757-A2.
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o;

Gaps

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cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or reating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                              VPCDKSFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLILGDDGHVKIADFGVSNQF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE 420
                                                                                                                                                                                                                                                                             LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder.
                                                                                                                                                                                                                                                                                               BEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
                                                                                                                                                                                                                                            DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ
                                                                                                                                                                                                                                                                                                                                                                             AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                                                                                                                                                                                                                                                                                                                            VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF
                                                                                                                                                                                                                               MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                                                                                                                                                                                                        0
                                   This invention describes novel human NOVX polypeptides which
                                                                                                                                                                                Length 505;
                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                 Query Match 99.1%; Score 2611; DB 5;
Best Local Similarity 99.4%; Pred. No. 3.9e-234;
Matches 502; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVKEGFGEGGKSPELPGVQEDEAAS 505
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            1; Page 139; 1103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein kinase #10.
                                                                                                                                    ABX97008-ABX97185
                                                                                                                                                            Sequence 505 AA;
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Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Batturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0299303P
2001US-0299310P
2001US-030454P
2001US-0312909P
2001US-0312903P
2001US-0318462P
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2001US-0325681P.
2001US-0330380P.
2001US-0333172P.
2001US-0332271P.
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2001US-033272P.
2001US-0332094P.
2001US-033746P.
2001US-0338092P.
2001US-0275579P.
2001US-0275601P.
2001US-0276000P.
2001US-027676P.
2001US-0276394P.
2001US-027733P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
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Casman SJ, Me
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2001US-0291240P.
2001US-0294485P.
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2001US-0294899P.
2001US-0299027P.
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2001US-0278999P.
2001US-0279036P.
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2001US-0277338P.
2001US-0279995F.
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2001US-0280802P.
2001US-0280802P.
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2001US-0288528P.
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2001US-0281194P.
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2001US-0287424P.
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N-PSDB; ABX97035.
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14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
21-NOV-2001;
                                   16-MAR-2001;
19-WAR-2001;
20-MAR-2001;
20-MAR-2001;
20-MAR-2001;
21-MAR-2001;
23-MAR-2001;
23-MAR-2001;
27-MAR-2001;
27-MAR-2001;
27-MAR-2001;
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02-APR-2001;
02-APR-2001;
04-APR-2001;
04-APR-2001;
30-APR-2001;
03-MAY-2001;
03-MAY-2001;
15-MAY-2001;
16-MAY-2001;
16-MAY-2001;
31-MAY-2001;
31-MAY-2001;
31-MAY-2001;
31-MAY-2001;
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19-JUN-2001;
19-JUN-2001;
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16-AUG-2001;
10-SEP-2001;
27-SEP-2001;
27-SEP-2001;
18-OCT-2001;
14-NOV-2001;
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03-DEC-2001;
04-DEC-2001;
  13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
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30-MAR-2001;
30-MAR-2001;
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300

240

180

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ANU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polymolleotides encoding protein kinase and the polymoptides may be used in the prevention, diagnosis and treatment of disease associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. disorders (e.g. disorders (e.g. disorders), inflammatory disorders (e.g. disorders), and reproductive disorders (e.g. disorders), and reproductive disorders (e.g. infertility).

Additionally, polymorleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polymeptides may be used as antigens in the production of antibodies cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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                                                                                                                                                                                                                                       diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
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                                                                                                                                                   Martinez R;
                                                                                                                                                                                                                                     Nucleic acids encoding human kinase polypeptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2595; DB 4; Length 513;
Pred. No. 1.3e-232;
0; Mismatches 1; Indels 1
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                                                                                                                                                 Manning G,
                                                                                                                                                                                                                                                                                              Claim 7; Fig 2; 433pp; English.
                                                       22-NOV-2000; 2000WO-US032085.
                                                                                     99US-0167482P
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Matches 503; Conservative
                                                                                                                                              Whyte D,
Clary D;
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                                                                                                                                                                                                        N-PSDB; AAS06710.
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WO200138503-A2
                                                                                                                 (SUGE-) SUGEN
                                                                                   24-NOV-1999;
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Flanagan P,
                           31-MAY-2001
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Best Local {
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NGEEPLPSEERHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREE 471
                                                                                                                                                                                                                                            Human kinase; PKIN-2; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinome; leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antiposiatic; neuroprotective; cytostatic; hepatotrophic; osteopathic; vasotropic; antianginal; anorectic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "ATP/GTP-binding site motif A (P-loop)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Tyrosine kinase catalytic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Protein kinase domain"
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/note= "Kinase protein beta"
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                                                              480 RSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS
                                                  RSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS
                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                          AAE04361 standard; protein; 513 AA
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P, Khan FA;
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14-JAN-2000; 2000US-0176107P.
21-JAN-2000; 2000US-0177731P.
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                                                                                                                                                                                                                      Human kinase (PKIN)-2.
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Yao MG, Lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145.
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412
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Claim 1; Page 104-105; 128pp; English

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The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its CDNA are useful for diagnosis, prevention and treatment of immune disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia, adult respiratory deficiency syndrome (AIDS), Addison's disease, anaemia, autoimmune had an advantagis, sportasis, autoimmune had an advantagis, autoimmune thyroiditis, multiple sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic
                                                                                                                                                                                                                                                                                                                                                      keracosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis; cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and hypertension; and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream sequences such as prometers and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germline gene therapy for treating the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mentioned disorders. The present sequence is human kinase (PKIN)-2
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Sequence 513 AA;

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351
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                                                                                                                                                   61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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                                                                                                                                                                                                                                                           DCVQLNQYKLQSEIGKVGLTDAYLQGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFP 180
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                                                                                                                                                                         1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                                                                                                                                                                                                                                                                                                                                   181 ŘŘPPPŘGSQAAQGEPAKQLLPLERVYQETAILKKLDHVNVVKLIBVLDDPAEDNLYLV-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 PFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK
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                                                                                                                                                                                                                           DCVQLNQYKLQSEIGK-----GAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFP
                                                                                                                                                                                                                                                                                                    172 RRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFD
                                                                                                                                                                                                                                                                                                                                                                                                 240 LLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKC
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                                                                                               LLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI
                                      Gaps
                                        10;
98.5%; Score 2595; DB 4; Length 513; llarity 97.9%; Pred. No. 1.3e-232; Conservative 0; Mismatches 1; Indels 10
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 Query Match
Best Local Similarity
Matches 503; Conserv
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AAU79458 standard; protein; 561 AA. 15-JUL-2002 (first entry) Human novel kinase 16002. AAU79458; RESULT 9 AAU79458 EXHX SX

New human transferase protein for diagnosing and treating disorders e.g. cancer, Alzheimer's disease, anorexia, diabetes and to identify numani, tumour, adenocatione, heematopoietic neoplastic disorder; carcinoma; tumour, adenocatione, heematopoietic neoplastic disorder; leukaemia; lymphoma; brain disorder; cerebral ischaemia; infection; meningitis; brain absess; acquire immunodeficiency syndrome; obesity; AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes; Parkinson's disease; Muntington's disease; motor neurone disease; parkinsolic disorder; anorexia nervosa; pain; inflammation; ischaemia; irritable bowel syndrome; hart disorder; myocardial infarction; blood vessel disorder; atherosclerosis; bone metabolism disorder; cancer; enzyme, 16002; kinase; cellular proliferative disorder; osteoporosis; haematopoietic disorder; arthritis. modulators for therapeutic use. Meyers RA, Silos-Santiago I; 03-AUG-2001; 2001WO-US024601. 01-SEP-2000; 2000US-0229299P. (MILL-) MILLENNIUM PHARM INC. WPI; 2002-351781/38. N-PSDB; ABK49563. WO200220800-A2 Homo sapiens 14-MAR-2002. 

The invention relates to an isolated human kinase polypeptide encoded by the DNAs designated 16658, 14223 and 16002 included are a host cell comprising the DnAs designated 16658, 14223 and 16002 included are a host cell composed are a not compared that a compand are a host cell compressing the protein, detecting the presence of the DNA in a sample comprising the protein detecting the presence of the DNA in a sample comprising contacting the sample with a compound which selectively hybridises to the DNA and determining whether the compound has bound and determining whether the compound has bound to and/or modulate the protein comprising contacting the protein with a test compound and determining whether the compound has bound to and/or modulated the function of the protein (the modulacrs may be a small molecule, a peptide, a comprising contacting the protein with a test compound and determining whether the compound has bound to and/or modulators and antibodies are useful in the diagnosis, monitoring and treatment of and antibodies are phosphopeptide, an antibody or a fragment of the full length protein). The nucleic acids, proteins, identified modulators and antibodies are useful in the diagnosis, monitoring and treatment of a wide range of diseases and disorders (may examples of which are listed in the specification) including cellular proliferative disorders (e.g. carebral ischaemia, infections such as mand nerve tissue disorders (e.g. cerebral ischaemia, infections such as the meningitis, brain abscress, acquired immunodeficiency syndrome (AlDS)-crelated myopathy, prion diseases, Allahamer's disease, metabolic crelated myopathy, prion diseases, and motor neurone disease, metabolic crelated myopathy, prion diseases and motor neurone disease, metabolic crelated with infection, inflammation ischaemia, irritable bowel creareoporosis) and haemacopoletic disorders of bone metabolism (e.g. arsociated with infection, inflammation ischaemia, irritable bowel creapenporosis) and haemacopoletic disorders of bone metaboli

Claim 4; Fig 16; 143pp; English.

Sequence 561 AA;

Gaps ; 0 Length 561; Indels Score 2591; DB 5; I Pred. No. 3.4e-232; 0; Mismatches 2; 98.4%; Best Local Similarity 99.6%; Matches 497; Conservative Query Match

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1 MEGGPAVCCODPRABLYERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 

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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
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                                                         DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ
                                                                                                                                                             DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQ
                                                                                          VPCDKPFSEEQARLYLRDVILGLEYLHCQXIVHRDIKPSNLLLGDDGHVKIADFGVSNQF
                                                                                                                                                  EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA
                                                                                                                                                                                   THRKIKNEPVVPPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
               LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                 AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                  VPCDKPPSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF
                                                                                                                                                                                             EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
                                                                                                                                                                                                                               EEHCSVVEVTEBEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
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2001US-0274194P.
2001US-0274281P.
2001US-0274322P.
2001US-0274849P.
2001US-0275534P.
2001US-0275579P.
2001US-0275601P.
2001US-0275601P.
2001US-027601P.
2001US-027601P.
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09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
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19-MAR-2001;
20-MAR-2001;
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21-MAR-2001;
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a disorder associated with aberrant NOVX expression or activity e.g
cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
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E, Kekuda R;
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2001US-0288342P
2001US-0291190P
2001US-0291099P
2001US-0294899P
2001US-0294899P
2001US-0294899P
2001US-0294899P
2001US-0299027P
2001US-0299027P
2001US-029903P
2001US-039310P
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2001US-039310P
2001US-0318770P
2001US-031890P
2001US-031890P
2001US-031890P
2001US-031890P
2001US-03330380P
2001US-03330380P
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2001US-0279344P.
2001US-0277338P.
2001US-02779995P.
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2001US-0332094P.
2001US-0337426P.
2001US-0338092P.
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2001US-0280802P.
2001US-0280822P.
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2001US-0283675P.
2001US-0287424P.
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2001US-0333184P.
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Gusev V,
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Zerhusen BD, G
Patturajan M,
Fernandes ER,
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18-0CT-2001; 2
31-0CT-2001; 2
14-NOV-2001; 2
14-NOV-2001; 2
14-NOV-2001; 2
14-NOV-2001; 2
21-NOV-2001; 2
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16-MAY-2001; 2
16-MAY-2001; 2
31-MAY-2001; 3
31-MAY-2001; 2
31-MAY-2001; 2
118-JUN-2001; 2
22-MAR-2001, 23-MAR-2001, 23-MAR-2001, 27-MAR-2001, 27-MAR-2001, 28-MAR-2001, 29-MAR-2001, 29-MAR-2001, 202-APR-2001, 202-APR-2001, 202-APR-2001, 202-APR-2001, 202-APR-2001, 202-APR-2001, 202-APR-2001, 202-MAY-2001, 203-MAY-2001, 203-MAY-20
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19-JUN-2001;
10-JUL-2001;
31-JUL-2001;
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10-SEP-2001; 2
12-SEP-2001; 2
27-SEP-2001; 2
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Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L; Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R; Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V; Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Ande: Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobri Lepley DM, Rieger DK,
08-MAR-2001; 2001US-0274101P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-02741321P.
09-MAR-2001; 2001US-0274849P.
12-MAR-2001; 2001US-0275234P.
13-MAR-2001; 2001US-0275234P.
13-MAR-2001; 2001US-0275234P.
13-MAR-2001; 2001US-0275234P.
13-MAR-2001; 2001US-0275234P.
14-MAR-2001; 2001US-0275234P.
15-MAR-2001; 2001US-0277321P.
16-MAR-2001; 2001US-0277321P.
16-MAR-2001; 2001US-0277321P.
17-MAR-2001; 2001US-0277321P.
18-MAR-2001; 2001US-0277321P.
18-MAR-2001; 2001US-0277321P.
19-MAR-2001; 2001US-0277321P.
19-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277321P.
11-MAR-2001; 2001US-0277338P.
11-MAR-2001; 2001US-0277338P.
11-MAR-2001; 2001US-0277338P.
11-MAR-2001; 2001US-0277338P.
11-MAR-2001; 2001US-0277338P.
11-MAR-2001; 2001US-0297302P.
11-MAR-2001; 2001US-0297310P.
11-MAR-2001; 2001US-0397310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001; 2001US-039310P.
11-MAR-2001
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                                                                                                                                                                                                            LIPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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 asthma. The products of the invention can be used for gene therapy or a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded b ABX97008-ABX97185
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                                                                                                                                                    1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                                                                                                                                                                     1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
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                                                                                                                        Gaps
                                                                                                                        38;
                                                                                         Length 543;
                                                                                                                       Indels
                                                                                         98.1%; Score 2585; DB 5;
92.4%; Pred. No. 1.2e-231;
iive 0; Mismatches 3;
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                                                                                                         Local Similarity 92.4
nes 502; Conservative
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                                                             Sequence 543 AA;
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                                                                                           Query Match
Best Local
                                                                                                                        Matches
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, Anderson D; Alsobrook JP;

protein kinase; eye;

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calcium/calmodulin-dependant
            retinoblastoma, brain, kinase modulator
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472; Conservative
  protein;
                                                                                                                                                                                                                       WPI; 2002-404955/43.
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                                                                                                                                                                          (PEKE ) PE CORP NY.
                                   Rattus norvegicus
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                                                          WO200224920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification
                                                                                                                                                                                                 Beasley EM,
  kinase
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Best Local Si
Matches 472;
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                                                                                                               This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or
                                                                                                                                                                                                                                                                                                                                                   LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
                                                                                                                                                                                                                                                                                                                                                                                                 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                              DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPARPSLSARKLSLOERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
                                                                                                                                                nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                       09
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                                    treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat amino acid sequence related to the kinase protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHRKIKNEPVVPPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                NOVX polypeptides and polynucleotides, useful for preventing or treatia disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEHCSVVEVTEEBVKNSVRLIPSWITVILVKSMLRKKSFGNPFEPQARREERSWSAPGNL
                                                                                                                                                                                                                                                                                                    1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                        Length 503;
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                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                         Score 2560; DB 5;
Pred. No. 2.2e-229;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505
                                                                                           Claim 1; Page 139; 1103pp; English.
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                                                                                                                                                                                                                                                         97.2%;
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                                                                                                                                                                                                                                                                    Best Local Similarity 98.2
Matches 496; Conservative
 2002-723332/78.
                                                                                                                                                                                                           ABX97008-ABX97185
          N-PSDB; ABX97034
                                                                                                                                                                                                                                   Sequence 503 AA;
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The invention relates to an isolated peptide designated human kinase

(HK), that has homology to members of the calcium/calmodulin-dependent
protein kinase kinase subfamily. The mechanism of action of the protein
of the invention is that of a kinase modulator. The human kinase of the
creating a disease or condition mediated by the human kinase. HK is also
useful to provide a target for diagnosing a disease or predisposition to
disease mediated by HK, and is also useful in pharmacogenic analysis. HK
is useful for treating a diseorder characterised by absence of
clisease mediated by HK, and is also useful in pharmacogenic analysis. HK
is useful for treating HK to a mammalian organism e.g. rat. rabbit
or mouse. Nucleic acide of the invention are useful as hybridisation
probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells
expressing a native HK are useful for assaying compounds that stimulate
or inhibit HK function. Nucleic acide of the invention are also useful
for producing transgenic animals. Experimental data indicates that kinase
proteins of the present invention are expressed in humans in the eye
creating sequence related to to kinase protein of the invention, appearing as
caid sequence related to to kinase protein of the invention, appearing as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 get for diagnosing
the peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide designated as human kinase useful
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                                                                                                                                                                                                                                                                                                          Sanders
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                                                                   19-SEP-2000; 2000US-0233493P.
13-NOV-2000; 2000US-0247031P.
06-DEC-2000; 2000US-00729995.
19-SEP-2001; 2001WO-US029161.
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector; a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the cctavity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the polynetides given in the specification, a method for identifying a compound useful in treating
EGNDAQLSSTAGTPAFMAPEALSDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
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                                                                                                                                                                                                                                                                                                                                        Rat, pain, neuronal tissue, gene therapy; spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury; SNI; Chung.
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                                  LHRKIKNEAVVPPEEPEVSEELKOLILKMLDKNPETRIGVSDIKLHPWVTKHGEEPLPSE
                                                                                                                                                                                                                                                                                              EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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GENBANK; AAB46910.
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pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VPCDKPFPEEQARLYLRDIILGLEYLHCOKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 APQGGPAKQLLPLERVYQEIAILKKLDHYNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                                                                                                                                                                                                                                                                                                  61 PIPVRPSLSARKFSLQERPAGSCLEAQVGPYSTGPASHMSPRAWRRPTIESHHVAISDTE
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                                                                                                                                                                                                                                                                                                                             61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKL.IEVLDDPAEDNLYLVFDLLRKGPVME
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                                                                                                                                                                                                                                   93.7%; Score 2468; DB 7; 93.5%; Pred. No. 8.5e-221;
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                                                                                                                                                                                                                                                                                           The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a gent that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially compound that regulates the activity of one or more of the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the expression of a method for identifying a compound useful in treating compound for identifying a compound useful in treating compolition comprising the one or more of the specification, a method for identifying a compound useful in treating compolities or the compound that compound that modulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is a fat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the proposition of the protein (shown in Table 2 of the specification, but was 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VPCDKPFPEEQARLYLRDIILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIPVRPSLSARKFSLQERPAGSCLEAQVGPYSTGPASHMSPRAWRRPTIESHHVAISDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCVQLNQYKLQSEIGKGAYGVVRLAYNEREDRHYAMKVLSKKKLLKQYGFPRRPPRGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APQGGPAKQLLPLERVYQETAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 2468; DB 7; Length 505;
; Pred. No. 8.5e-221;
11; Mismatches 22; Indels
                                                                                                                                            Costigan M;
                                                                                                                                             Befort K,
                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.7%;
                             14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P.
14-AUG-2002; 2002WO-US025765.
                                                            26-NOV-2001; 2001US-033347P
                                                                                          (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 472; Conservative
                                                                                                                                          Woolf C, D'urso D,
                                                                                                                                                                         2003-268312/26.
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Best Local Similarity
                                                                                                                                                                                          GENBANK; AAB46910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 505 AA;
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Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; Addison's disease; multiple sclerosis.
EEHCSVVEVTEEEVKNSVKLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNI, 480
                                                                           LHRKIKNEPVVFPEEPEISEELKOLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                                                                                    EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Potential phosphorylation site"
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462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Potential phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Potential phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Potential phosphorylation
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/label= Signature_sequence
                                                                                                                                                                                                                                                                                         LVKEGFGEGGKSPELPGVQEDEAAS 505
                                                                                                                                                                                                                                                                                                                       LLKEGCGEGGKSPELPGVQEDEAAS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44239 standard; protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cell signalling protein-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
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CDNA obtained from Instructure close 640521 of BRSTNOTO3 library. It is expressed in reproductive, nervous and developmental tissues and is found to be homologous to Ca2+fcalmodulin-dependent protein kinase kinase. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders associated diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders like AIDS, Addison's disease, multiple sclerosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 YGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIAILKKLOHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCDKPFSEEQARLYLRD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 LIKGIEYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPAFMA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is cell signalling protein-2 (CSIGP-2) encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LDSSGSQ---ARPHLSGRKLSLQERSQGGLAAGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 EADGGPEPTRNGVDPPPRARAASVIPGSTSRLLPARPSLSARKLSLQER----PAGSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 BAQAG-----PYATGPASHISPRAWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 VILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFEGNDAQLSSTAGTPAFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 PEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVFPEEPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.4%; Score 1537.5; DB 3; Length 540; Best Local Similarity 62.0%; Pred. No. 5.6e-134; Matches 300; Conservative 79; Mismatches 74; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cell signaling proteins useful for, e.g. diagnosing cell proliferative and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                     Patterson
                               'note= "Potential phosphorylation site"
note= "Potential phosphorylation site"
                                                                     'note= "Potential phosphorylation
                                                                                                      /note= "Potential phosphorylation
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                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                 Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 64-65; 90pp; English
                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                        99WO-US010567
                                                                                                                                                                                                                                           98US-0085343P.
                                                                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                               Hillman JL,
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                                                                                                                                                                                                                                                                                                                                                     Yang J;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 540 AA;
              Modified-site
                                               Modified-site
                                                                                  Modified-site
                                                                                                                                        WO9958558-A2
                                                                                                                                                                                                          13-MAY-1999;
                                                                                                                                                                                                                                           13-MAY-1998;
26-AUG-1998;
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Baughn MR,
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        QY
        379 SEELKDLILKMLDXNPETRIGVPDIXLHPWVTKNGEBPLPSEEEHCSVVEVTEGEVKNSV 438

        Db
        416 AEDLKDLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEEEHCSVVEVTEGEVRNSV 475

        QY
        439 RLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGEGGKSPELPGV 498

        Db
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        QY
        499 EDE 502

        Db
        535 GEEB 538
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Search completed: July 12, 2004, 04:50:08 Job time : 106 secs

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AY416155 Pan trogl
AL539375 AL539375
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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BG294573 603391909
BU571280 NISC 1207
BI546778 603191356
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CB712914 AMGNNUC:N
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Sheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Homo sapiens CAMKKI gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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BQ571613 U
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BI819446 6
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BG396486
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Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus CAMKKI gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                        CTGCTCCTGGGGGATGATGGCCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT
                                                 CTGCTCGTGGGGGATGATGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT
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2 (bases 1 to 1518)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murina;
I (bases Le 1518)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal;
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                      /locus_tag="HCM5796"
                                                                          Location/Qualifiers
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/gene="CAMKK1"
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Best Local Similarity 99.7%;
Matches 1511; Conservative
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Pan troglodytes CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Pan troglodytes
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Pan.
1 (bases I to 1445)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Adams, M.D. and Cargill, M.
Inferting nonneutral evolution from human-chimp-mouse orthologous gene trios
                                         CTGGGCCTCGAGTACTTGCACTGCCAGAAGATTGTCCACAGGGACATCAAGCCATCTAAC
                                                                                                                                                                    GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGAACCCCAGCATTCATGGCCCCCGAG
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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Warg,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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80.7%; Score 1222.6; DB 29; Length 1518;
Best Local Similarity 87.4%; Pred. No. 9.7e-260;
Matches 1324; Conservative 0; Mismatches 191; Indels 0; (
                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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AL539375 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF033X017 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12868532.
Contact: Genoscope
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           14671302
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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0; Mismatches 381; Indels

    11445
organism="Pan troglodytes"

 Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9598"
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/gene="CAMKK1"
/locus_tag="HCM5796"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Library was constructed by Life Technologies, a division of
Library May Genoscope.cns.fr/
Contact:
Forgibling Email: fliangelifetech.com URL:
Contact:
Attps://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Ayenue Genoscope sequence ID: CSODK012BD11QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LA401350 Thomo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK012YG22 5-PRIME, mRNA sequence.

BX401350
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                                                                                                                                                                                                                                                                                                                                                                                                                 965 GGAACGACGTCAGCTGTCCAGCACGGGGAA-CCCAGCATTCATGGCCCC--GAGGCA
                TGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAGGGGCCCCGTCATGGAAGTGCC
                                           TGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAAGTGCC
                                                                                                     CTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATCCTGGG
                                                                                                                                               CCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAACCTGCT
                                                                                                                                                                                                                           CCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAACCTGCT
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/cell_line="HELA"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone="CS0DK012YG22"
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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             Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF033AH09QPl&cluster=8786.r. Contact
Feng Liang Email: filangalifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF033AH09QPl.
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Best Local Similarity 97.2%; Pred. No. 3.3e-197;
Matches 1005; Conservative 5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                     tissue_type="FETAL BRAIN"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODF033Y017"
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                                                                                                                                                                                 GETGTEGGACCCCCCCCCACAGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA
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                                                   ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
                                                                            ATGGAGGGGGTCCAGCTGTCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
                                                                                                          GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC
                                                                                                                                                              GGTGTGGACCCCCCCCCACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA
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BX395129 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens

BX395129 LOCUS DEFINITION

RESULT

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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY coedex. France
Bmail: segret@genoscope.ms.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitorgen. This sequence belongs to sequence cluster 8786.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODD001AC08QPl&cluster=8786.r. Contact:
Feng Liang Email: fliang@ilfetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD001AC08QPl.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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5; Mismatches 2;
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E. (Dases 1 to 1096)

S. NIH-MGC http://mgc.nci.nh.gov/.

Inthylished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov
Plate: LLAM12724 row: a column: 07
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AGENCOURT_6499735 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728398
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                          <u> AAAAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG</u>
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                                                                                                                                       GCCATCCTGAAGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC
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                                                           GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGGTGTACCAGGAGATT
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/tissue_type="hippocampus"
/lab_host="DH10B"
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Location/Qualifiers
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/db_xref="taxon:9606"
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BM805189
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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                                                                                                                                                              Score 779.4; DB 12;
Pred. No. 1.2e-161;
0; Mismatches 52;
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93.1%;
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517

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577

1344

697

637

1404

757

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapba-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAMIO725 row: a column: 07
High quality sequence stop: 769.
Location/Qualifiers
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                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 80 Na.

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                       AGCACGGCGGGAACCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGC
                                                                                                                                                                                                                                                                                                                                                                    398 GGGAAGTGCCCGTTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAG
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Matches 815; Conservative
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/note="Vector: pCMV-SPORT6" (Life Technologies); Site_1:
Directionally cloned using the following adaptors:
5'-TCGACCACGCTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
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AGAA-GATCGTCCACA-GGGACATCAAGCCATCCAACCTGCTCCTGGGGGATGATGGGCA
                                                                                                                                                                                                                                                                                                                                                     AGENCOURT 8805197 Lupski sciatic nerve Homo sapiens cDNA clone IMACE:6196986 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Produrement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3606 row. e column: 19
High quality sequence stop: 577.
Location/Qualifiers
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Pred. No. 3.4e-151;
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6196986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                          CGTGAAGATCGCCGACTTTGGCGT 887
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94.4%;
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                                                                                                                   /clone_lib="NIH MGC_95"
/clone_lib="NIH MGC_95"
/clone_"Crgan: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (grcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2:5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coh 49.0%; Score 742.4; DB 12; Length al Similarity 95.7%; Pred. No. 1.6e-153; 827; Conservative 0; Mismatches 31; Indels
/db_xref="taxon:9606"
/clone="IMAGE:4820238"
/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches 827
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/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into BcoRI/KhoI sites using the following 5, adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Bupersecript II RT (Life Technologies). Note: this is a
NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAGTGCCCATTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAG 1104
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   Score 723; DB 13;
Pred. No. 3.6e-149;
); Mismatches 15;
                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5804754"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
                                                          GIGGCCAICTCAGAIGCAGAGGACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGGTGAG
                                                                                                                                                                                                                  GAGCGGGTGTACCAGGAGATTGCCATCCTGAAGAGCTGGACCACGTGAATGTGGTCAAA
TCCCTACAGGAGCGGCCAGCAGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACG
                                     GGGCCTGCCACACATCTCCCCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCAC
                                                                                                            GTGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAG
                                                                                                                                                                                    ATTGGCAAGGGTGCCTACGGTGTGGTGAGGCTGGCCTACAACGAAAGTGAAGACACAC
                                                                                                                                                                                                                                                          TATGCAATGAAAGTCCTTTCCAAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGC
                                                                                                                                                                                                                                                                                        TATGCAATGAAAGTCCTTTCCAAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGC
                                                                                                                                                                                                                                                                                                                              CCTCCCCGAGAGGGTCCCAGGCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                 GAGCGGGTGTACCAGGAGATTGCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENCOURT 7048118 NIH MGC_109 Homo 5', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCo
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1302 row: 1 column: 04
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602459214F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4581651 5'
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NIH-MGC http://mgc.nci.nih.gov/.
National Intsitutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xef="txxxx:9606"
/clone="IMAGB:4581651"
/tissue_type="retinoblastoma"
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High quality sequence stop: 733
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 972)
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   696 CTGGGGAAGTCCATGCTGAAGGAAGCGTTCCTTTGGGAACCCTTTGAGCCCCAAGCACG
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF003DB02QP1.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r
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/clone_lib="Homo sapiens FETAL_BRAIN"
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/tissue_type="FETAL BRAIN"
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/db_xref="taxon:9606"
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                                                                                                                                                                           13;
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Pred. No. 1.8e-142;
0; Mismatches 34;
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COT 25-NORMALIZED Homo sapiens
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Li, Wass, Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /note="lst strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOBAG049ZH12_CSO4704_1&cluster=8786.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG049ZH12_CSO4704_1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 680.6; DB 13;
Pred. No. 8.1e-140;
0; Mismatches 19;
                                                                                                                                 BX328136

896 bp mRNA
8328136 Homo sapiens HELA CELLS COT 25-
CDNA clone CSODK012YG22 5-PRIME, mRNA se
BX328136
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/db_xref="taxon:9606"
/clone="CS0DK012YG22"
                                                                                                                                                                                                                          BX328136.1 GI:30338689
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96.9%;
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Matches 726; Conserv
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AUTHORS
TITLE
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                                                                                      RESULT 14
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gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Nor I sitte. Double stranded cDNA was pize fraction.

Oligo-dT primer containing a Nor I sitte. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into PXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Amatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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UI-M-FC0-byc-e-19-0-UI.rl NIH_BMAP_FC0 Mus musculus cDNA clone
IMAGE:5716218 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/clone_lib="NIH_BMAP_FCO"
/note="Organ: brain; Vector: pXX-Asc; Site 1: EcoR I;
Site 2: Not 1: The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1307 ACTCAGTCAGGCTCATCCCCAGCTGGACCACGGTGATCCTGGTGAAGTCCATGCTGAGGA
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                                                                                                                                                               CAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAAAAATCCCGAGA
                                                                                                                                                                                                                                                                                                                                       CGAGAATTGGGGTGCCAGACATCAAGTTGCACCCTTGGGTGACCAAGAACGGGGAGGAGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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APPLICANT: WEI, Ming-Hui et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND U

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: 05/10/135,689

CURRENT APPLICATION NUMBER: 60/247,031

PRIOR FILING DATE: 2000-01-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASLEGO for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: WEIL STATE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/135,689
CURRENT FILING DATE: 2002-05-01
 ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
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TITLE OF INVENTION: ACID MOLECULES ENCODI
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOD904
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTER OF FOR Windows Version 4.0
SEQ ID NO 3
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PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 09/729,995
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
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; ORGANISM: Human
US-09-729-995-3
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APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS,
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; Sequence 3, Application US/09729995
; Patent No. 6426206
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Patent No. 6500338

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                           4
                                                                                                                 Length 288;
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                              DB 4;
                                                                                                            Score 142.8; DB 4
Pred. No. 1.7e-27;
0; Mismatches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Zeller, Karen J. RESTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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al Similarity 70.7%;
203; Conservative (
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
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IMMEDIATE SOURCE:
                     ; LIBRARY: BRAIN; CLONE: 926034
US-09-016-434-1008
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Best Local
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                  ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PARRAACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHYNE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1008:
SEQUENCE CHARACTERISTICS:
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

~WESTER: IBM PC compatible

~WESTER: TOWN: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLASSIFICATION:
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                                                                                       Greaagaagaarrcaacracreaggaggrracggcacaaaargrcarccagcregg
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                                           586 GIGIACCAGGAGALIGCCAICCIGAAGAAGCIGGACCACGIGAAIGIGGGICAAACIGAIC
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Gaps
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Sequence 1146, Application US/09016434

Batent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                       646 GAGGICCIGGAIGACCCAGCIGAGGACAACCICIAITIGGIGIIIGA
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
  Mismatches
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CITY: PALO ALTO
  Conservative
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                                                                                                                                                                                                                                                           20 AAGGGCCCGTGGATGGAAGTGCCCACCCTTNAAACCACTCTCTGAAGACCAGGNCCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                     GGGACATCAAGCCATCCAACCTGCTCCTGGGGGATGATGGCGCACGTGAAGATCGCCGACT
                                                                                                                                                                                                             703 AAGGGGCCCGTCATGGAAGTGCCC-TGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCT
                                                                                                                                                                  Gaps
                                                                                                                                                                  2;
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                                                                                                                    Length 236;
                                                                                                                                                               59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 Tridercheadchardantreahddecherdacdcdc 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVESTION: DNA ENCODING PROTEIN KINASE NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NOTICE.
                                                                                                               Score 99.4; DB 4;
Pred. No. 2.3e-16;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90.4; DB 1;
Pred. No. 9.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            881 TIGGCGICAGCAACCAGITIGAGGGGAACGACGCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BROWDY AND NEIMARK, P.L.L.C. 419 7th Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP PCT/JP96/00660 FILING DATE: 15-MAR-1996
ATTONNEY/AGENT INFORMATION:
NAME: YUM, Allen C.
REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,050A
FILING DATE: 05-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 57104/1995
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08913050A
Patent No. 5827726
GENERAL INFORMATION:
APPLICANT: NEZU, Jun-ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                      6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                 Query Match 6.6
Best Local Similarity 71.8
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    ; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT03
; CLONE: 531037
US-09-016-434-809
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Best Local Similarity
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GIGIACCAGGAGATIGCCATCCTGAAGAAGCTGGACCACGTGAATGTGTGTCAAACTGATC 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 GTGAAGAAAATTCAACTACTGAGGAGGTTACGGCACAAAATGTCATCAGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 GATGTGTTATACAACGAAGGAAGCAGAAATGTATATGGTGATGGAGTACTGCGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 AGAAAGGGGCCCGTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 CTCTACCTGCGGGACGTCATCCTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCAC
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                                                                                                                                                                                                                              GENERAL INPORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 87; DB 2; Le
ilarity 50.0%; Pred. No. 7.7e-13;
Conservative 0; Mismatches 310;
                                                                                                                                                                                                                                                                                                                                                                                                     3: INCYTE PHARMACEUTICALS, INC. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOMATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0150 US
                                                                                                                                                                        US-08-749-902-2
; Sequence 2, Application US/08749902
; Patent No. 5985635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELEPHONE: 415-855-0555
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IBM Compatible
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MEDIUM TYPE: Diskett
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STRANDEDNESS: sing
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Best Local Similarity
Matches 331; Conserv
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                                                 AA 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586 GIGIACCAGGAGATIGCCAICCIGAAGAAGCIGGACCACGIGAAIGIGGICAAACIGAIC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 GIGAAGAAGGAAATICAACTACTGAGGAGGTTACGGCACAAAAATGTCATCCAGCTGGTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 BIDDIDD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 90.4; DB 4; Length 1302;
Pred. No. 9.7e-14;
0; Mismatches 306; Indels 21
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                                                                                                                                                                                                                                                    PA-0002 US
CURRENT APPLICATION DATA: US/09/016,434
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PA.00
TELECOMMUNICATION:
TELEPHONE: (650) 845-0555
TELEPAX: (650) 845-4166
INPOMATION FOR ESC ID NO: 1146:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
                                                                                                                                                                                                                              37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.0%;
Best Local Similarity 50.6%;
Matches 335; Conservative
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                      APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                            HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: 91480860
US-09-016-434-1146
                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                        FILING DATE
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2160 CAGCGACGTGTTCTCTGAGCCCCGTGCCATCTTTTATTCCGCCTGCGTGCTGCTGGGCCT 2219
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                                                                                                                                                                                                                                                                2280 GGACACCGAGGGCTACGTCAAGATCGCAGACTTTGGCCTCTGCAAGGAGGGGATGGGCTA
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                                                                 789 CGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAACCTGCTCCT
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
FILE REFERENCE: RTS-0035
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Pred. No. 6.7e-12;
0; Mismatches 226;
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CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09256465 Patent No. 6043090
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AAGGGCATCAAGCCGGGGGAACCTGCTGACCACCGGTGGCACCCTCAAAATCTCCGAC
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                                                                                                    980 TITGGCGTCAGCAACCAGTTTGAGGGGAACGACGCTCAGCTGTCCAGCACGGC
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APPLICANT: MAIBULIT, KOZO
APPLICANT: ONO, YOSHITAKA
APPLICANT: ONO, YOSHITAKA
APPLICANT: INAWATSU, AKHHRO
TITLE OF INVENTION: MODIFIED PROTEIN DERIVED FROM PROTEIN KINASE N
FILE REPERENCE: 016897/0844
CURRENT FILING DATE: 1996-07-24
CURRENT FILING DATE: 1996-07-24
PRIOR APPLICATION NUMBER: UP 7-262552
PRIOR APPLICATION NUMBER: UP 7-344606
PRIOR APPLICATION NUMBER: UP 8-080549
PRIOR FILING DATE: 1996-03-08
PRIOR APPLICATION NUMBER: UP 8-114226
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PRIOR APPLICATION NUMBER: UP 8-114226
PRIOR FILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.1
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Patent No. 6660837
GENERAL INFORMATION:
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; LOCATION: (37)..(2862)
US-08-685-852-1
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                                                                                                                                                                                    1066 GATTICATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAG 1125
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Pred. No. 6.7e-12;
0; Mismatches 226; Indels 15
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1004, Application US/09023655 Patent No. 6607879
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
ITLE OF INVENTION: COMPOSITION FOI
ITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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Best Local Similarity 51.3
Matches 254; Conservative
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STRANDEDNESS: single
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LIBRARY: GENBANK
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US-09-023-655-1004
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US-09-023-655-1004
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1198 GCACGCTCAGCCCCGAGGCCAAGTCCCTGCTTGCTGGGCTGCTTAAGAAGGACCCCCAAG 1257
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                                                                                                                                                                                                                                                                                 APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. TITLE OF INVENTION: CANCER VACCINE NUMBER OF SEQUENCES: 14 CORRESONDENCE ADDRESS: And ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cch 5.5%; Score 83.4; DB 4; Length 1
al Similarity 51.3%; Pred. No. 6.7e-12;
254; Conservative 0; Mismatches 226; Indels
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NAME: MOLGO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-0ct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      Sequence 3, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
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                                                                                                              1258 CAGAGGCTTGGTGGG 1272
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STRANDEDNESS: single
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                                                                   1186 ACGAGAATTGGGGTG
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US-09-167-322-3
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Best Local 3
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946 ITCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGAT 1005
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271 TACTCCTTCCAGGAC---GAGGAGGACATGTTCATGGTCGTGGACCTGCTACTGGGCGGG 327
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                                                                                                                              766 CIGCGGGACGICATCCIGGGCCICGAGIACTIGCACTGCCAGAAGAICGICCACAGGGAC
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                                                                          GGGCCCGTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTAC
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APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721e1 Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REPERBICE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 6/182,059
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 2000-09-12
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Pred. No. 1e-11;
0; Mismatches 192; Indels 6
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6638721
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Conservative C
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US-09-799-875-13
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ORGANISM: Homo sapiens
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses;
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/209996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR FILING DATE: 2000-09-12
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
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Matches 224; Conservative (
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; ORGANISM: Homo sapiens
US-09-799-875-15
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Db 404 ATCTGCGAGATGGCTCTGGACTGCTGCGCGCCACATCATCCACAGAT 463

QY 826 ATCAAGCCATCCAACCTCTGGAGATGATGGCACGTCAACATTGGC 885

Db 464 GTCAAGCCTGACAACTTCTCTGGATGAGAGACATGCACCTGACCGACTTTGGC 885

QY 886 GTCAGCAACCATTCTCTGGATGAGAGAGACACTCCAGCACCTGACCGACTTCAAC 523

QY 886 GTCAGCAACCATTCTCTGATGAGGAACGACGGGGGAAACCCCAGCA 945

Db 524 ATTGCCACCATCATCAAGGC--ACGGGGAGCGGCGATTAGCAGCCCAGCA 580

QY 946 TTCATGGCCCCCGAGGCATTTCTGATTCCGGCAGAGCGCAAGCCG 580

QY 1006 GT 1007

Db 641 GT 642
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Search completed: July 25, 2004, 11:37:16 Job time : 147 secs

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Abals566 Human kin
Abx11551 Human pol
Abx47035 Human NOV
Abk49563 Human CDN
Aas06710 Polynucle
Aad06835 Human kin
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Listing first 45 summaries
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24	25	26	27	00	29	30	31	32	33	34	32	36	37	38	0.00	0.4	41	4.2	43	44	45			RESULT 1	ABL58698

Human; kinase protein; calcium/calmodulin-dependant protein kinase; eye; retinoblastoma; brain; kinase modulator; gene; SNP; single nucleotide polymorphism; ss. Human kinase encoding cDNA. (first entry) 27-AUG-2002 ABL58698 

/product= "human kinase" replace(1296, G) Location/Qualifiers /*tag= a 173. .1690 *tag= b .172 Homo sapiens variation Key 5'UTR

/*tag= c /standard_name= "single nucleotide polymorphism" 1691. .2190 /*tag= d Di Francesco V; Sanders R, Bonazzi VR, 19-SEP-2000; 2000US-023493P. 13-NOV-2000; 2000US-0247031P. 06-DEC-2000; 2000US-00729995. 19-SEP-2001; 2001WO-US029161 Beasley EM, Wei M, (PEKE ) PE CORP NY WO200224920-A2 28-MAR-2002 3'UTR

Novel peptide designated as human kinase useful as target for diagnosing WPI; 2002-404955/43. P-PSDB; ABB83054.

> Human cDN Human pro DNA encod

AAS27190

The invention relates to an isolated peptide designated human kinase

(HK), that has homology to members of the calcium/calmodulin-dependent

protein kinase kinase subfamily. The mechanism of action of the protein

of the invention is that of a kinase modulator. The human kinase of the

creating a disease or condition mediated by the human kinase of the

creating a disease or condition mediated by the human kinase. HK is also

useful to provide a target for diagnosing a disease or predisposition to

disease mediated by HK, and is also useful in pharmacogenic analysis. HK

cuseful for treating a disorder characterised by absence of

inappropriate or unwanted expression of HK, also as an immunogen to raise

antibodies by administering HK to a mammalian organism e.g. rat, rabbit

or mouse. Nucleic acids of the invention are useful as hybridisation

probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells

expressing a native HK are useful for assaying compounds that stimulate

or inhibit HK function. Nucleic acids of the invention are also useful

for producing transgenic animals. Experimental data indicates that kinase

proteins of the present invention are expressed in humans in the eye

(retinoblastomas) and brain. The current sequence represents cDNA. a disease or predisposition to the disease mediated by the peptide. Fig 1; 89pp; English 4p; Claim 

Sequence 2190 BP; 457 A; 655 C; 708 G; 370 T; 0 U; 0 Other;

0 ATGGAGGGGGTCCAGCTGTTGCTGCTGCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG 232 120 180 352 240 412 472 360 532 420 592 480 652 540 712 600 772 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 660 1 ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG GGTGTGGACCCCCACCACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGA GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC GGTGTGGACCCCCCACACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA CCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG CTGCTCCCAGCCCAAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCA CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGACGTGGCCATGCAGAG AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGAGAGGGTCCCAG AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCCCCTGGAGCGGGTGTACCAGGAGATT GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC GTGGTGAGGCTGGCTACAACGAAGTGAAGACAACAACAACAAGAAGTCCTTTCC GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGTGTACCAGGAGTT GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT Gaps 0; DB 6; Length 2190; Indels 0; .0%; Score 1515; Mismatches 0; 100.0%; Best Local Similarity 100.
Matches 1515; Conservative 773 233 293 241 Query Match 173 61 121 181 353 413 301 473 533 653 713 601 361 421 593 541 481 d δ g g QQ  $\delta$ Dp à Dp à õ à Q ò q ð a

g ₹  $\delta$ 

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ð í	21	8
9 2	ν ₋	ITCICGGAGGAGCAGCTCGCCTCTACCTGCGGGACGTCATC 95
2 4	53	CTGGGCCTCGAGTACTTGCACTGCCAGAAGTCGTCCACAGGGACATCAAGCGATCCAAC  CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC  1012
δ	841	CCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT 90
qq	1013	CGTGAAGAICGCCGACTTTGGCGTCAGCAACCAGTTT
δλ	901	
qq	1073 (	AGGGAACGAACGCTCAGCTGTCCAGCACGGCGGAACCCCAGCATTCATGGCCCCCGAG
Sy Op	961 (	GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGCCTTGGATGTATGGGCCACTGGC 1020
ð í	21	AAGTGCCCATTCATCGACGATTTCATCCTGGCC 108
Q C	1193	CACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCT
à i	н .	CCGTGGTGTTCCTGAGGGCCAGAAATCAGCGAG 114
a C	53	DACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG 131
کم بر د	1141 (	INCITAGACAAGAATCCCGAGACGAGAATTGGGGTG
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<u> </u>	1373 (	CCASACATCAAGTIVCACCCTTGGGTGACCAAGAAGGGGGAGGAGCCCCTTCCTT
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g qq	333	GAGGAGCACTGCACCGTGGTTCATTTTTTTTTTTTTTTT
ò	21	GCTGGACCACGGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 138
Ob	93	Ŋ
Š	81	AACCGTITGAGCCCCAGGCACGGAGGGAAAAGCGATCCATGTCTCCAGGAAACCTA 1440
QQ	1553 A	CCGTTTGAGCCCCAGGCACGGAGGAAGAGCGATCCATGTCTGCTCCAGGAAA
δλ	1441 C	TGGTGAAAGAAGGGTTTGGTGAAGGGGGCAAGAGCCCAGAGCTCCCCGGCGTCCA
q	1613	TGGTGAAAGGAGGGTTTGGTGAAGGGGGGAAGAGCCCCAGAGCTCCCCGGCGTCCAG
δ	1501 G	CGAGGCTGCATCC 151
QQ	73	GAGGCTGCATCC 16
RESU AAD3 ID	LT 2 0566 AAD3056	tandard; cDNA; 1937 BP.
A S	030566	
il X	21-MAY-200	2 (first entry)
XX	Human kina	se polypeptide (PKIN-19) cDNA.
<b>™</b>	Human; kin	nase polypeptide; PKIN-19; gene therapy; Addison's disease;

m

leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; daucher's disease; myocardial infarction; drug screening; transgenic animal; antinflammatory; hepatotropic; hypotensive; anti-HIV; enzyme; ss.

Homo sapiens

/product= "Human PKIN-19" Location/Qualifiers 65. .1582 /*tag=

WO200208399-A2

31-JAN-2002

20-JUL-2001; 2001WO-US023092

21-JUL-2000; 2000US-0220038P. 28-JUL-2000; 2000US-0222112P. 04-AUG-2000; 2000US-0222831P. 11-AUG-2000; 2000US-0224729P

(INCY-) INCYTE GENOMICS INC.

(THOR/) THORNTON M.

Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK; Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR; Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L; Yao MG, Bllict VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR; Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;

WPI; 2002-206083/26.

P-PSDB; AAE19161.

New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.

Claim 5; Page 193-194; 196pp; English.

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, I wasful for diagnosing, treating and preventing cancer (e.g., leukaemia, I ymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis, a growth and developmental disorder (e.g., anterosciency), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial inflarction), and a lipid disorder (e.g., fatty liver, cholestasis, daucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting canimals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting cell effected individuals, and as hybridisation celtc, among normal, carrier or affected individuals, and as hybridisation correct mapping naturally occurring genomic sequences. PKIN is useful technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising continuation occurrances. present sequence is human PKIN-19 cDNA

Sequence 1937 BP; 425 A; 567 C; 603 G; 342 T; 0 U; 0 Other;

Gaps Score 1510.2; DB 6; Length 1937; Pred. No. 0; 0; Mismatches 3; Indels 0; Query Match 99.7%; Best Local Similarity 99.8%; Matches 1512; Conservative

·.

y da	1 ATGGAGGGGGTCCAAGCTGTCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG 60
δλ	1 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 1
Dp	5 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 1
è é	121 GGTGTGGACCCCCCACCACGGCCCACAGCTGCCTGTGTGATCCCTGGCAGTACTTCAAGA 180
ò	1 CIGCTCCCAGCCCGGCCTAGCCTCTCAGGAAGCTTTCCCTACAGGAGCGAGC
qq	
δλ	TATCTGGAGGCGCAGGTGGGCCTTATGCCACGGGGCCTGCCAGCCA
ΩD	5 GGAAGCTATCTGGAGGGGCAGGCTGGGCCTTATGCCACGGGGCCTGCCAGCCA
oy S	SECTEGECEGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG :
2 2	00 CECECGGGECELGGEGGGGGGGGCCGAECGGGGGGGGGGG
40 q0	25 GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTTGAGAATTGGCAAGGGTGCCTACGGT 4
δλ	TGSTGAGGCTGGCCTACAACGAAGTGAAGACACACTATGCAATGAAAGTCCTTTCC 4
qq	TGGCCTACAACGAAAGTGAAGACAGACATTTGC 5
οχ	1 AAAAAAAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG 5
Ωp	5 AAAAAAAATTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGCTCCCAG 6
Qy	CTGGAGCGGGTGTACCAGGAGATT 6
QΩ	CTGCCCAGGGAGCACCAGCCAAGCAGCTGCTGCCCCTTGGAGCGGTGTACCAGGAGTT 6
QY	GGATGAC 6
qa	CATCCTGRAGAAGTTGGACCACGTGATGTGGTCAAACTGATCGAGGTCCTGGATGAC
δλ	1 CCAGCTGAGGACAACCTCTATTTGGTGTTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA 7
qq	CIGAGGACAACCICTATIIGGIGIIIIGACCICCIGAGAAAGGGGCCCGICAIGGAA 7
δλ	TTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC 7
qq	TGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC 8
δλ	781 CIGGGCCTCGAGTACTTGCACTGCCAGAGAGTCGTCCACAGGGACATCAAGCCATCCAAC 840
ОD	medeccicedatacinecacreccadaacarcercacacacarcaaccarccarc
Qy	GCCGACTTTGGCGTCAGCAACCAGTTT 9
qq	5 CIGCICCIGGGGGAIGAIGAGGCACGIGAAGAICGCCGACTIIGGCGICAGCAACCAGIII 9
Qy	TGTCCAGCACGCCGGAACCCCAGCATTCATGGCCCCCGAG 96
ηD	AGGGGAACGATCAGCTGTCCAGCACGGCGGGAACCCCAGCATTCATGGCCCCCGAG
δλ	1 GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGAAGGCCTTGGATGTATGGGCCACTGGC 102
Db	CCATITICIGATICCGGCCAGAGCTICAGIGGGAAGGCCTIGGAIGIAIGGGCCACIGGC 108
δλ	CGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCA
qq	85 GICACGIIGIACIGCIIIGICIAIGGGAAGIGCCCGIICCAICGACGAIIICAICCIGGCC 114

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-625 ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABE6890-ABE68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellopielle-conformation of a proliferative disorders (cancer), neurodegenerative diseases (Parkinson's proliferative disorders (anoter), neurodegenerative disorders, diseases), autoinfunne diseases (multiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parassitic), arthritis, etc. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGGCCTACTAGAAAC 120
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genetic, myeloid or lymphoid, or platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2018 BP; 453 A; 600 C; 603 G; 362 T; 0 U; 0 Other;
                                                                                         SEQ ID NO 433; 1012pp + Sequence Listing; English
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Pred. No. 0;
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autoimmune,
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                                    coagulation disorders.
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Matches 1510; Conservative
neurodegenerative,
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                                    Li L;
R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1505.4; DB 6; Length 1611; Pred. No. 0; 0; Mismatches 6; Indels 0;
                              Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Gusev V, Ji W, Gorman L, Miller CE, Kekuda Gangolli E, Vernet CAM, Guo X, Tchernev V; Casman SJ, Malyankar UM, Gerlach V, Liu Y, Catterton E, Burgess C, Leite M, Zhong H, A
                                                         Kekuda
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                                                                                                                                                                                                                                                                                                                               1103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 1509; Conservative
                                Spytek KA,
Gusev V,
                                                                                                                                Rieger DK
CURAGEN CORP
                                                                                                                                                                       WPI; 2002-723332/78.
                                                                                                                                                                                                                                                                                                                               Page 139;
                                                                                                                                                                                         P-PSDB; ABU65068
                                  Padigaru M, Sp
Zerhusen BD, G
Patturajan M,
Fernandes ER,
                                                                                                                Spaderna SK,
                                                                                                                                  Lepley DM,
                                                                                                                                                                                                                                                                                                                               Claim 13;
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Human; ss; gene; 16002; kinase; cellular proliferative disorder; cancer;
                                                           carcinoma; tumour; adenocarcinoma; haematopoietic neoplastic disorder; leukaemia; lymphoma; brain disorder; cerebral ischaemia; infection; meningitis; brain abscess; acquire immunodeficiency syndrome; obesity; AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes; Parkinson's disease; Huntington's disease; motor neurone disease; metabolic disorder; anorexia nervosa; pain; inflammation; ischaemia; irritable bowel syndrome; heart disorder; more disease; blood vessel disorder; atherosclerosis; bone metabolism disorder; osteoporosis; haematopoietic disorder; arthritis.
                                  Human cDNA 16002 encoding a novel kinase
                                                                                                                                                                         iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-351781/38.
P-PSDB; AAU79458.
                                                                                                                                                                                                                                        WO200220800-A2
                                                                                                                                                       Homo sapiens,
                 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                 Meyers RA,
ABK49563;
                                                                                                                                                                         Key
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/product= "Kinase 16002" /note= "This coding sequence (minus the stop codon) is specifically claimed in claim 1" 198. .1883 ď /*tag=

03-AUG-2001; 2001WO-US024601

01-SEP-2000; 2000US-0229299P

Silos-Santiago I;

New human transferase protein for diagnosing and treating disorders e.g. cancer, Alzheimer's disease, anorexia, diabetes and to identify modulators for therapeutic use.

Claim 1; Fig 16; 143pp; English.

The invention relates to an isolated human kinase polypeptide encoded by the DNAs designated 16658, 14223 and 1602 including fragments, chomologues and allelic variants. Also included are a host cell comprising the DNA, an antibody which selectively binds to the novel kinase, a method for producing the novel kinase comprising culturing the host cell and recovering the protein, detecting the presence of the DNA in a sample comprising contacting the sample with a compound which selectively hybridises to the DNA and determining whether the compound has bound and identifying compounds which bind to and/or modulate the protein comprising contacting the protein with a test compound and determining whether the compound has bound a cand/or modulate the function of the protein (the modulators may be a small molecule, a peptide, a phosphopeptide, an antibody or a fragment of the full length protein). The uncleic acids, proteins, identified modulators and antibodies are useful in the diagnosis, monitoring and treatment of a wide range of diseases and disorders (many examples of which are listed in the specification) including cellular proliferative disorders (e.g. cancers of the lung and breast; carcinomas, tumours, adenocarcinomas, haematopoietic neoplastic disorders e.g. leukaemias and lymphomas), brain and nerve tissue disorders (e.g. cerebral ischaemia, infections such as meningitis, brain abscess, acquired immunodeficiency syndrome (AIDS)-related myopathy, prion diseases, Alzheimer's disease, Parkinson's disease, Huntingron's disease and motor neurone disease) metabolic disorders (e.g obesity, anorexia nervosa and diabetes) pain disorders (e.g. associated with infection, inflammation ischaemia, irritable bowel syndrome), heart disorders (e.g. myocardial infarction), blood vessel

1098 GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGGAACCCCAGCATTCATGGCCCCCGGAG 1157

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disorders (e.g. atherosclerosis), disorders of bone metabolism (e.g. osteoporosis) and haematopoietic disorders (e.g. arthritis). The present
                                                                                                                                                                                                            198 ATGGAGGGGGTCCAGCTGTCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
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                                                                      C; 848 G; 508
                                                                                                       Score 1490.6;
                                                                                                                       Pred. No. 0;
0; Mismatches
                                   sequence encodes novel human kinase 16002
                                                                      Sequence 2711 BP; 592 A; 752
                                                                                                     98.4%;
Similarity 99.4%;
96; Conservative
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Matches 1496;
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AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides corrected the conding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of disease associated with carecter (especially cancers of hematopoietic origin), cardiovascular cancers (especially cancers of hematopoietic origin), cardiovascular disease (e.g. atherosis), metabolic disorders (e.g. diabetes), infamantors of sorders (e.g. diabetes), infamantory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase against the protein kinase sand in assays to identify modulators of protein kinase expression and activity
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                             encoding human kinase polypeptides, useful for preventing 1/or treating e.g. cancer, immune, cardiovascular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCCATCGATGTGACTCACTTGGAGGAGGAGGAGATGGTGGCCCAGAGCCTACTAGAAAC
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neuronal-associated diseases, and microbial infections.
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Best Local Similarity 97.98;
Matches 1510; Conservative
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                             GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its cDNA are useful for assessing toxicity of a test compound. PKIN and its cDNA are useful for assessing toxicity of efficiency syndrome (AIDS), Addison's disease, anaemia, adult respiratory distress syndrome, allergies, amyloidosis, psoriasis, autoimmune thyroiditis, multiple sclerosis, asthma, acteoathritis, osteoaptrosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and Mypertension; and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences such as promoters and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germline gene therapy for treating the above mentioned disorders. The present sequence is human kinase (PKIN)-2
               Human kinase; PKIN-2; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
                                                                   leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression
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Pred. No. 0;
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P, Khan FA;
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14-JAN-2000; 2000US-0176107P-
28-JAN-2000; 2000US-01731P-
28-JAN-2000; 2000US-01735P-
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Best Local Similarity 97.99
Matches 1509; Conservative
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Tao MG, Lal
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ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTGAGAACGGGTG

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CDNA; 3501

AAD08635 standard;

RESULT 7 AAD08635

Human kinase (PKIN) -2 cDNA

(first entry)

04-SEP-2001

AAD08635;

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us-10-690-617-1 copy 173 1687.rng

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Claim 13; Page 138; 1103pp; English.
                           2001US-0280802P
2001US-028082P
2001US-0280900P
2001US-0281494P
2001US-0281424P
2001US-0288666P
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P-PSDB; ABU65067.
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02-APR-2001; 2
02-APR-2001; 2
04-APR-2001; 2
13-APR-2001; 3
30-APR-2001; 2
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19-JUN-2001;
10-JUL-2001;
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18-OCT-2001; 3
31-OCT-2001; 3
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31-MAY-2001;
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16-AUG-2001;
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14-NOV-2001;
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21-NOV-2001;
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Anderson D; Alsobrook JP; Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L; Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R; Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V; Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Ander Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrc Lepley DM, Rieger DK; NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial

cytostatic, cardiant, antiarteriosclerotic, affiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX9708-3185 are CDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97185. This invention describes novel human NOVX polypeptides which have ABU65041-ABU65218

120 420 439 480 499 540 009 619 099 139 180 240 259 300 319 360 619 720 780 900 916 736 856 09 79 140 GGTGTGGACCCCCCACCACCACCACGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA 200 CIGCICCCAGCCCAGCCICICAGCCICICAGGAAGCITICCCTACAGGAGGGGGCCAGGA 260 GGAAGCTATCTGGAGGCCCAGGCTGGGCCTTATGCCACGGGGCCTGCCAGCAACTACCCC CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTCCCTGGAGCGGGTTACCAGGAGTT 620 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTACTGGATGAC GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC 20 AradadadadactactacracracracadarccradacagacadanaaAcadara GCAGCCATCGATGTGACTTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 80 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 320 CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 380 GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC 440 GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG 500 AAAAAGGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGGTCCCAG GCTGCCCAGGGAGGACCAAGCAACAGCTGCTGCCCTGGAGCGGGTGTACCAGGAGATT GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC creadcercagagracarcreccagaagarcerccacagagacarcaagccarccaac GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGGAACCCCAGCATTCATGGCCCCCGAG GAGGGGAACGACGCTCAGCTGTCCAGCACGCGGGAACCCCAGCATTCATGGCCCCCGAG 1 ATGGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG CTGCTCCCAGCCCGGCCTAGCCTCTCAGCAAGCTTTCCCTACAGGAGCGGCCAGCA GCCATCCTGAAGATGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC CCAGCTGAGGACCACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGGACATCAAGCCATCCAAC CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT GGTGTGGGACCCCCCCCCACCACGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT Gaps Length 1547; 9 A; 441 C; 474 G; 280 T; 0 U; 0 Other; Indels DB 6; 17; Score 1455.8; Pred. No. 0; 0; Mismatches Query Match Best Local Similarity 98.5%; Matches 1492; Conservative Sequence 1547 BP; 352 089 917 ( 301 560 601 857 737 61 121 181 241 361 421 481 541 661 721 781 797 841 901 196  $\delta$ g qq Db XX ò g g ò d δ g  $\delta$ qq ð Db  $\delta$ d  $\delta$ g ò g ò q à ò ò ò q ò d ð ð g

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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
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                 2001US-0277321P
2001US-027737P
2001US-0277791P
2001US-0278152P
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2001US-0278899P
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                20-MAR.2001; 20-MAR.2001; 20-MAR.2001; 22-MAR.2001; 23-MAR.2001; 27-MAR.2001; 27-MAR.2001; 28-MAR.2001; 29-MAR.2001; 29-MAR.2001; 29-MAR.2001; 20-APR.2001; 202-APR.2001; 
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03-MAY-2001;
03-MAY-2001;
15-MAY-2001;
16-MAY-2001;
16-MAY-2001;
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13-MAY-2001;
11-JUN-2001;
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GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAG---TTGGATGTATGGGCCACTGGC
                                                                                                  CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
                                                                                                                                                                      GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG
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                                                                                                                                 1094 CTCCACAGGAAGATCAAGAATGAGCCCGTGGTTTTCCTGAGGAGCCAGAAATCAGCGAG
                                  GICACGITGIACTGCITIGICIAIGGGAAGIGCCCAITCAICGACGAITICAICCIGGCC
                                                       CTGGTCAAAGAGGGTTTGGTGAAGGGGGCAAGAGCCCAGACTCCCCGGCGTCCAGGAA
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08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274281P.
09-MAR-2001; 2001US-0274849P.
13-MAR-2001; 2001US-027523F.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275601P.
14-MAR-2001; 2001US-027600P.
16-MAR-2001; 2001US-027600P.
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activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX9708-ABX97185 are CDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97993. ABX97084-BCR canced the NOVX proteins described in
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                                                                                                                                                                                                                                                                                                                                                                                                Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.
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2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
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                                                                                                     CTGGTGAAAGAAGGGTTTGGTGAAGGGGGCAAGAGCCCAGAGGCTCCCCGGCGTCCAGGAA 1500
                                                                                                                    The present sequence is a cDNA obtained from Incyte clone 640521 of BRSTNOT03 library. It encodes cell signalling protein-2 (CSIGP-2). It is expressed in reproductive, nervous and developmental tissues. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP each be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with prevention and treatment of CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like atteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders like AIDS, Addison's disease, multiple sclerosis, etc
                                  1427 ATCCCCAGCTGGACCACTGTGATCCTGGTCAAGTCTATGCTGAGAAAGCGTTCCTTTGGA 1486
                                                                                                                                                                                                                                                                                                                             Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; Addison's disease; multiple sclerosis; ss.
            ATCCCCAGCTGGACCACGGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG
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                                                                                                                                                                                                                                                                                                       Human cell signalling protein-2 encoding cDNA
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                                                            Length 2545;
506 T; 0 U; 0 Other;
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                                                            Score 660.2; DB 3;
Pred. No. 2.3e-154;
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Sequence 2545 BP; 542 A; 737 C; 760 G;
                                                                                              Best Local Similarity 71.3%;
Matches 885; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to newly discovered cancer markers associated with
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for
                                                                                                                       GGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGGTTTGGTGAAGG
            GACAGAGGGGGGGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACGGTGATCCT
                                 GACTGAAGAGGGGTCGAGAACTCAGTCAAACACATTCCCAGCTTGGCAACCGTGATCCT
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                                                                             GGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTCGAGGGC---AGCCGGCG
                                                                                                                                                                                                                                                                                                            Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
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diagnosing and treating prostate cancer in mammals. The prostate cancer-
associated genes are useful for diagnosing or treating prostate cancer,
as well as for identifying modulators of prostate cancer or agents that
inhibit prostate cancer. The nucleic acid sequences are particularly
useful in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
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Pred. No. 3.9e-152;
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nes 871; Conservative
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Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                               Score 651; DB 9;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38649-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous injuries, peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic alteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                          GAAGTGCCCATTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCC 1106
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	I nucleic - nucleic search, using sw model	nn on: July 24, 2004, 22:25:04 ; Search time 9534 Seconds (without alignments) 6887.424 Million cell updates/sec	Title: US-10-690-617-1_COPX_173_1687 Perfect score: 1515 Sequence: 1 atggagggggtccagctgtaggaagacgaggctgcatcc 1515	oring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	arched: 3470272 segs, 21671516995 residues	otal number of hits satisfying chosen parameters: 6940544	nimum DB seq length: 0 wimum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	tabase : GenEmbl:*  1: gb ba:*  2: gb btg:*  4: sb on:*  5: gb_ov:*  6: gb_pa:*  10: gb_r:*  11: gb_si:*  11: gb_si:*  11: gb_si:*  12: gb_ov:*  13: gb_un:*  14: gb un:*  15: em_ba:*  15: em_ba:*  16: em_uni:*  17: em_uni:*  18: em_uni:*  19: em_uni:*  22: em_ov:*  23: em_si:*  24: em_si:*  25: em_vi:*  25: em_vi:*  26: em_vi:*  27: em_si:*  28: em_tig_inv:*  29: em_vi:*  29: em_vi:*  31: em_htg_inv:*  32: em_htg_inv:*  33: em_htg_inv:*  34: em_htg_inv:*  35: em_htg_inv:*  36: em_htg_inv:*  37: em_htg_inv:*  38: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  39: em_htg_inv:*  40: em_htg_inv:*  40: em_htg_inv:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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173   ATGGAGGGGGTCCAGCTGTTGCTGCTGGGATCCTTGGGGAGCTGGTAGAACCGGTG   232	AGCA AGCA CTCC CTCC	301 CCCCGGGCCTGGCGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG 360		601 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAACTGATCGAGGTCCTGGATGAC 660 773 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 6832 661 CCAGCTGAAGACAACCTCTATTTGGTGTTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA 720	721 GTGCCCTGTGACAAGCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC 780		1133 GCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGCCATGGC 1020 1133 GCCATTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC 1192 1021 GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC 1080 1193 GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC 1252 1081 CTCCACAGGAAGATCAAGAATGAGGAAGTGCCCATTCCTCAAGGAGCCCAGAAATCAGCGGG 1140 1253 CTCCACAGGAAGATCAAGAATGAGAGCCCGTGGTGTTTCCTCGAGGAGCCAGAAATCAGCGAG 1140 1253 CTCCACAGGAAGATCAAGAATGAGGCCCGTGGTGTTTCCTGAGGAGCCCAGAAATCAGCGAG 1312

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Lasses 1 to 3536)
Tascedda,F., Carra,S., Harvey,M. and Barden,N.
Characterization of human CaMKK alpha gene structure
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2 (bases 1 to 3536)
Tascedda,F., Carra,S., Harvey,M. and Barbiret Submission
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Reggio Emilia, Campi 183, Modena, MO 41:
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/codon_start=1
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
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                                                                                                    Gaps
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                                                                                                    2; Indels
                                                                        DB 9;
                                                                        Score 1511.8;
Pred. No. 0;
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Best Local Simi
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Eukaryota, Maraca, Chordata, Craniata, Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 3575)
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschni, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha, transcript variant 1, mRNA (cDNA clone MGC:49844

MAGE:551570), complete cds.
                           942 CTGCTCCTGGGGGATGATGGCCACGTGAAGATCGCCGACTTTGGCGTCAACCAGTTT
                                                                                                         1002 GAGGGGAACGACGTCAGCTGTCCAGCACGCGGGAACCCCAGCATTCATGGCCCCCGAG
                                                                                                                                              GCCATTTCTGATTCCGGCCACAGGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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/tanslation="MeGGPACCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDP
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KKKLLKQYGPRRPPRPRGSQAAQGGPAKQLLPERVYQEIAILKKLDHYNVKLIFVL
DDPAEDNLYLVPDLLRKGPVWEVPCRPFSEEQARLYLEDVIIGLEYLHCQKIVHRDI
KRSNLLIGDOGHYKLADFGVSKQFEGNDAQLSSTAGFPAFMAPEAISDSGQSFSGKAL
UNWATGVTLXCFVYGKCPFIDDFILALHRKIKNEPVVPPEEPRISEELKDLILKMLDK
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PPRARAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPR
AWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLS
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DDPAEDNLYLVPDLLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDI
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DVMATGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVFPEBPEISEELKDIILKMLDK
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KSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGGGGKSPELPGVQEDEAAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Link at: http://image.llnl.gov series: IRAK Plate: 89 Row: h Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27437009. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dannes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Isai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-70-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11803, Bethesda, MD 20892-2590,
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/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="synonyms: DKFZp761M0423, CAMKKA, MGC34095
                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/product="calcium/calmodulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha, isoform a"
/protein_id="AAH43487.1"
/db_xref="GI:27694084"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 3575)
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REFERENCE
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TITLE
JOURNAL
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please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVL
DDABDNILYTVTVPLLAKGPYMEVPCRFRESEGARLVIRDVILGLEYLTGQKYYHRDI
KPSNLLLGDDGHVKLADFGYSWQFESNDAQLSSTAGTPAFMAPEAISDSGSFSGKAL
DVMATGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVPPEEPBISELEKOLILKMIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPETRIGVPDIKLHPWVTKNGEEPLPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILV
KSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS"
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                       host
                            Braunschweig/Germany) within the cDNA sequencing consortium of German Genome Project.
This clone is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 ATGGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGTGGCCCAGAGCCTACTAGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="amygdala"
/clone_lib="761 (synonym: hamy2). Vector pSportl;
DH10B; sites NotI + SalI"
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                                                                                                                                                                                                                                       /mol_type="mRNA"
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/db_xref="tzxpn:9606"
/db_xref="txpn:9606"
/db_xref="txpn:9606"
/clone="DKFZp761M0423"
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Pred. No. 0;
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                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="DKFZp761M0423"
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gene="DKFZp761M0423"
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Best Local Similarity 99.9°
Matches 1513; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecher, M., Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Kochrer, K., Strack, N., Mewes, H.W., Outerwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A.
Toward a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs Genome Res. 11 (3), 422-435 (2001)
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Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                        GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC
                                                                                                                                                                                         CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
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                       GCCATITCTGATICCGGCCAGAGCTICAGIGGGAAGGCCTIGGAIGIAIGGCCACIGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTGAAAGAAGGGTTTGGTGAAGGGGGCAAGAGCCCAGAGCTCCCCGGCGTCCAGGAA
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Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens mRNA; cDNA complete cds.
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RESULT

SOURCE

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465   CTGGTGAGGCTGGCCTA.CAACGAAAGTGAAGACACACACATATGCAAGTGAAGTCCTTTCC   481   AAAAAGAGTTTCTGAAGCAGTGCTGCCCTGCCCCGCGGGGGGTCCCCGG   481   AAAAAGAGTTTCTGAACCAGTTTCCCCCTGCCCCTGCCCCCCGGGGGGTCCCCGG   481   AAAAAGAGTTTATTCTGAACCAGTTTCCCCCTGCCCCTGCCCCCCGGGGGGTCCCCGG   481   CTGCCCCGGGGAAGACTGCCTGTGACTCCTCCCCCGGGGGGGG	TITICC 544	540 RESULT 8 AX455763 604 LOCUS AX455763	DEFINITION   CONTROL   C	SOURCE 660 ORGANISM 724	REFRENCE 720 AUTHORS TITLE 784 GOURNAL	780 FEATURES SOURCE	840 ORIGIN	0 -			OY 241 GGAAGCTATCTGGAGG 	Qy         301 CCCGGGCCTGGGGAA           1260         Db           11				Qy   S41 GCTGCCCAGGGAGGAC 	3
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PAT 06-JUL-2002 ö 180 240 480 CTGGACCACGTGAATGTGGTCAACTGATCGAGGTCCTGGATGAC 660 120 120 180 240 300 300 360 360 420 420 480 540 540 600 600 09 09 a, Chordata, Craniata, Vertebrata, Buteleostomi, a, Primates, Catarrhini, Hominidae, Homo. AAGCAGTATGGCTTTCCACGTCGCCCTCCCCGGAGAGGTCCCAG Silos-Santiago,I. 11602, novel human kinases and uses therefor 184 9 14-MAR-2002; INC (US) GCTGTCTGCCAGGATCCTCGGCCAGAGCTGGTAGAACGGGTG GCTGTCTGCTGCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG ACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC GCGCAGGCTTGATGCCACGGGGCCTGCCAGCCACATCTCC GCGCAGGCTGGGCCTTATGCCACGGGGCCTGCCAGCCACATCTCC AGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG AACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT TACAACGAAAGTGAAGACAGACTATGCAATGAAAGTCCTTTCC TACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC CCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGTGTACCAGGAGATT CCACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA CCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCA CAGCCAAGCAGCTGCCCCTGGAGCGGGTGTACCAGGAGATT AACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT Gaps Score 1490.6; DB 6; Length 1683; Pred. No. 9.6e-312; 0; Mismatches 9; Indels 0; linear DNA m="Homo sapiens" e="unassigned DNA" i="taxon:9606" 1683 bp Patent WO0220800. /Qualifiers 714790 4 4 % % lan)

AUTHORS Meyers R.A. and Silos-Santiago, I.  TITLE 16659, 14223, and 16002, novel human kinases and uses therefor JOHNAL PRESENT WOOD CARDON AT 14-WAR - 2002; RILLARING HAMA INC [03] FEATURES  LOCATION FRAM INC [03]  LOCATION FRAM INC [03]  LOCATION FRAM INC [04]  LOCATION FRAM INC [05]  LOCATI	498 361 558 618 618 678 678 678 678
CCAGCTGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA	OY 1441 CTGGTGAAAGAAGGGTTTGGTGAAGGGGGAAGAGCCCAGAGCTCCCGGGGTCCAGGAA 1500  Db 1441 CTGGTGAAAGAAGGGTTTGGTGAAGGGGCAAGAGCCCAGAGCTCCCGGCGTCCAGGGT 1500  QY 1501 GACGA 1505  Db 1501 TACCA 1505  NA455761  LOCUS  ACCESSION  AX455761  AX455761  AX455761  AX455761  AX455761  AX455761  AX455761  BEFINITION  ACCESSION  AX455761  AX455761  AX455761  AX455761  BENARYORDS  SOURCE  Homo sapiens (human)  ORGANISM Homo sapiens (human)  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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n.G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., an,P. and Clary,D.S.
human protein kinases and protein kinase-like enzymes
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ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                   1. .1542
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xxef="taxon:9606"
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Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SOURCE ORGANISM

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larity 97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang,J., Baughn,M.R., Burford,N., Au-Young,J., Lu,D.A., Reddy,R., Yue,H., Yao,M.G., Lal,P. and Khan,F.A.
Human kinases
Patent: No.0146397-A 14 28-JUN-2001;
Incyte Genomics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                           AACGGGGAGGAGCCCTTCCTTCGAGGAGGAGCACTGCAGCGTGGTGGAGGTGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAGGITAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACGGTGATCCTGGTGAAG
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                                                            GGAACCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGG
                                                                                                                  GGAACCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGG
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                                                                                                                                                               CCATTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCCGTGGTG
                                                                                                                                                                                                                 TITICCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC
                                                                                                                                                                                                                                                                        TITCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC
                                                                                                                                                                                                                                                                                                    AAGAATCCCGAGACGAGAATTGGGGTGCCAGACATCAAGTTGCACCCTTGGGTGACCAAG
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GTCCACAGGGACATCAAGCCATCCAACCTGCTCGTGGGGGATGATGGGCACGTGAAGATC
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Catarrhini; Hominidae;
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|mol_type="unassigned DNA"
|db_xref="taxon:9606"
|note="Incyte ID No: 2041716CB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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Sequence 14 from Patent WO0146397.
AX179641
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Primates;
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   Location/Qualifiers
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Mammalia; Eutheria;
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AX179641
LOCUS
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KEYWORDS
SOURCE
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Clone distribution: MGC clone distribution information can be found
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PPRARAASVI PGSTSRLLPARPSLSARKLSLOERPAGSYLEAQAGPYATGPASHISPR
AWRRPTIESHHVAISDAEDCVQLNQYKLOELGRAGVYVEAANTEBSBCHYAMKVLS
KKKLLKQYGFPRRPPERGSQAAGGRAKCLEPLERVYGEIAILKKLDHVNVKKLIEVL
DDPAEDNLYLALQNQAQNIQLDSTNIAKPHSLLPSEQODSGSTWAARSVFDLLRKGPV
MEVPCNKFFSEEQARLYLRDVTLGLEYLACQKTUHRDIKPSNILLGDDGHVKTADFGY
SNQFEGNDAQLSSTAGTPFAMAPEAISDSGGSFSGKALDVWATGVILYCFYGKCPFI
DDFILALHKKIRNERSPWFPEGPBISBELKDLILKMLDKNPFRIGGPTKCHPWYTKR
GEEPLPSEEEHCSVVFPEGFBISBELKDLILKMLDKRPPETRIGVPTKLHPWYTKR
GEEPLPSEEEHCSVVFFEEDVRNSVRLIFSWTTVILVKSMLRKRSFGNPFEPQARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 51 Row: 1 Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27437010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-JJM-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGAGGGGGTCCAGCTGCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NIH MGC_115"
/lab host="Wh10B"
/note="Vector: pCMV-SPORT6"
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catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/product="calcium/calmodulin-dependent protein kinase
alpha, iseform b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels 114; Gaps
                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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note="synonyms: DKFZp761M0423, CAMKKA, MGC34095"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:34095 IMAGE:5175128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAH31647.1"
/db_xref="GI:21594836"
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Best Local Similarity 92.0°
Matches 1453; Conservative
                                                                                                                            Direct Submission
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                                                                                         Strausberg, R.
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                            PUBMED
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JOURNAL
MEDLINE
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Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheafer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wnzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Blouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2469 bp mRNA linear PRI 06-OCT-2003 HOmo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha, transcript variant 3, mRNA (cDNA clone MGC:34095 IMAGE:5175128), complete cds.
                                                   1113
                                                                                                                                                                               TTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1173
                                                                                                                                                                                                                                                                                                               1202 TITCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1261
                                                                                                                                                                                                                                                                                                                                                                                     AAGAATCCCGAGACGAGAATTGGGGGTGCCAGACATCAAGTTGCACCCTTGGGTGACCAAG 1233
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2469)
                                                                                                                                         CCATTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCCGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1262 AAGAATCCCGAGAGCGAGAATTGGGGTGCCAGACATCAAGTTGCACCCTTGGGTGACCAAG
                   AAGGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTGTCTATGGGAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1414 CGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGGTTTGGTGAAGGGGGGCAAG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC031647.1 GI:21594835
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Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy,
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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/mol type="mRNA"
/strain=FVB/N"
/db_xref="tracn:10090"
/clone="MGC:27706 IMAGE:4924656"
/tlssue type="Salivary gland, 10 week old female mouse"
/clone lib="NCI CGAP_SG2"
/lab_host="DH10B"
                                  Bethesda, MD 20892-2590,
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catalytic domain"
/db_xref="CDD:smart00220"
        National Cancer
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                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nip.gov
Tissue Procurement: Jeffery E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.9%; Score 1241.4; DB 10; Length 3435;
88.7%; Pred. No. 6.7e-258;
iive 0; Mismatches 171; Indels 0;
     Cancer Genomics Office,
                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     George Yang, Scott Zuyderduyn, Marco Marra.
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                         Center Drive, Room 11A03,
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/protein_id="AAH17529.1"
/db_xref="GI:17028424"
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/db xref="LocusID:55984"
/db_xref="MGI:1891766"
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PPRARAAS VI PGSASR PTPVRPSLSARKFSLQBRPAGSCLEAQVGPYSTGPASHMSPR
AWRRPTI BSHHVAISDTBOUVQLNQYKLQSEI GKGAYGVVRLAYNERBDRHYAMKULS
KKKLLKQYGPPRRPPRGSQAPQGGPAKQLALBLERVYQBIA ILKKLDHVNVVKLI BVL
DDPABDNLYLVPDLLRKGPWBEVPCDKPFPBEQARLYLRDI ILGLEYLHCQKIVHRDI
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Sciurognathi, Muridae, Murinae,
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Okuno, S., Kitani, T. and Fujisawa, H.
Bvidence for the existence of Ca2+/calmodulin-dependent protein
Kinase IV Kinase isoforms in rat brain
J. Blochem. 119 (6), 1176-1181 (1996)
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GACCTCAAAGACCTGATCCTGAGGATGCTAGACAAGAATCCTGAGACAAGAATTGGGGGTG
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entry [NCBI gibbsq 179633] from the original journal article.
This sequence comes from Fig. 1.
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'/gene="Ca2+/calmodulin-dependent protein kinase IV isoform, CaM-kinase kinase alpha"
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/note="This sequence comes from Fig. 1,
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/product="Ca2+/calmodulin-dependent
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/protein_id="AAB46910.1"
/db_xref="GI:1836161"
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/db_xref="taxon:10118"
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                                                                                                                                   Length 3429
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                                                                                                                            Score 1238.2; DB 10;
Pred. No. 3.3e-257;
); Mismatches 173; Ii
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alpha, Cam kinase kinase alpha"

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/db_xref="G1:4512334"
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                                                                                                                                                                                                                                              KKKLLKQYGFPRRPPRGSQAPQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVL
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Pred. No. 7.4e-257;
0; Mismatches 174; Indels
/mol type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain"
/tissue_lib="brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                               /note="18 a nucleotides"
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Best Local Similarity 88.5%;
Matches 1341; Conservative
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Rattus norvegicus mRNA for Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha, complete cds.
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Evidence for the existence of Ca2+/calmodulin-dependent protein
kinase IV kinase isoforms in rat brain
J. Biochem. 119 (6), 1176-1181 (1996)
                                                                                                               GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG
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Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase
               GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
                                                                                       GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC
                                                                                                                                                              CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3411)
Pujisawa, H. and Okuno, S.
Direct Submission
Submitted (15-FEB-1999) Hitoshi Fujisawa, Asahikawa Medical
College, Department of Blochemistry; Nishikagura 4-5-3-11,
Asahikawa 078-8510, Japan (E-mail:ckuno@asahikawa-med.ac.jp,
Tel:+81-166-68-2340, Fax:+81-166-68-2349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
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